Table AMB. Probe Name Ag6427

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	462
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	463
Reverse	5'-ccctggatgcccatc-3'	15	1484	464

Table AMC. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	465
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	466
Reverse	5'-gggagccggtcagca-3'	15	899	467

Table AMD. Probe Name Ag6434

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctttgatggtgatgggaa-3'	19	1372	468
Probe	TET-5'-cttcatctaccatgggagcagcctg-3'-TAMRA	25	1394	469
Reverse	5'-gctcgggatgcccac-3'	15	1461	470

Table AME. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6434, Run 269253996	Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6434, Run 269253996
AD 1 Hippo	20.0	17.3	Control (Path) 3 Temporal Ctx	12.9	9.2
AD 2 Hippo	48.0	33.0	Control (Path) 4 Temporal Ctx	19.8	13.8
AD 3 Hippo	11.6	3.4	AD 1 Occipital Ctx	16.2	8.4

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AD 4 Hippo	17.1	9.0	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	39.2	66.4	AD 3 Occipital Ctx	11.7	3.8
AD 6 Hippo	**100.0**	**100.0**	AD 4 Occipital Ctx	12.6	1.4
Control 2 Hippo	17.9	23.3	AD 5 Occipital Ctx	16.7	21.3
Control 4 Hippo	38.4	26.6	AD 6 Occipital Ctx	17.8	15.5
Control (Path) 3 Hippo	10.2	7.0	Control 1 Occipital Ctx	11.3	5.5
AD 1 Temporal Ctx	12.1	13.7	Control 2 Occipital Ctx	24.8	33.7
AD 2 Temporal Ctx	36.6	35.8	Control 3 Occipital Ctx	16.4	3.0
AD 3 Temporal Ctx	11.7	7.2	Control 4 Occipital Ctx	12.1	8.1
AD 4 Temporal Ctx	15.6	6.7	Control (Path) 1 Occipital Ctx	32.8	39.0
AD 5 Inf Temporal Ctx	43.8	21.9	Control (Path) 2 Occipital Ctx	9.6	4.2
AD 5 SupTemporal Ctx	56.6	31.6	Control (Path) 3 Occipital Ctx	8.4	3.2
AD 6 Inf Temporal Ctx	40.9	52.9	Control (Path) 4 Occipital Ctx	15.9	9.3
AD 6 Sup Temporal Ctx	44.1	71.2	Control 1 Parietal Ctx	15.2	10.1
Control 1 Temporal Ctx	11.9	10.3	Control 2 Parietal Ctx	39.5	43.5
Control 2 Temporal Ctx	16.7	16.2	Control 3 Parietal Ctx	14.5	15.9
Control 3 Temporal Ctx	13.0	8.5	Control (Path) 1 Parietal Ctx	33.4	24.8
Control 4 Temporal Ctx	18.9	13.6	Control (Path) 2 Parietal Ctx	20.0	22.1
Control (Path) 1 Temporal Ctx	32.5	29.9	Control (Path) 3 Parietal Ctx	15.0	9.3

Control (Path) 2 Temporal Ctx	19.5	13.2	Control (Path) 4 Parietal Ctx	28.3	34.6

Table AMF. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6427, Run 277222437	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6434, Run 277222451
Adipose	0.0	0.0	8.2	9.5
Melanoma* Hs688(A).T	0.0	0.0	0.5	0.9
Melanoma* Hs688(B).T	0.0	0.0	0.6	3.7
Melanoma* M14	0.0	0.0	0.7	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	22.5	14.7
Squamous cell carcinoma SCC-4	0.0	0.0	0.3	0.0
Testis Pool	0.0	0.0	4.2	5.7
Prostate ca.* (bone met) PC-3	0.0	0.0	1.0	1.5
Prostate Pool	0.0	0.0	8.5	4.2
Placenta	0.0	0.0	0.1	0.5
Uterus Pool	0.0	0.0	2.6	2.5
Ovarian ca. OVCAR-3	0.0	0.0	0.8	0.8
Ovarian ca. SK-OV-3	0.0	0.0	1.5	0.8
Ovarian ca. OVCAR-4	0.0	0.0	0.5	0.5
Ovarian ca. OVCAR-5	0.0	0.0	1.5	2.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	90.8	73.7
Ovarian ca. OVCAR-8	5.6	0.0	11.9	20.7
Ovary	0.0	0.0	2.1	4.0
Breast ca. MCF-7	0.0	0.0	0.4	0.5
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.5
Breast ca. BT 549	0.0	0.0	0.3	0.5
Breast ca. T47D	0.0	0.0	0.3	0.0

Breast ca. MDA-N	0.0	0.0	0.7	0.0
Breast Pool	0.0	0.0	19.5	9.6
Trachea	0.0	0.0	2.9	5.3
Lung	0.0	0.0	1.3	1.3
Fetal Lung	0.0	0.0	4.0	5.0
Lung ca. NCI-N417	2.0	0.0	2.7	3.0
Lung ca. LX-1	3.1	0.0	7.0	4.3
Lung ca. NCI-H146	0.0	0.0	0.5	0.0
Lung ca. SHP-77	2.3	0.0	6.3	4.9
Lung ca. A549	0.0	0.0	0.3	0.7
Lung ca. NCI-H526	0.0	0.0	0.7	0.0
Lung ca. NCI-H23	0.0	0.0	4.5	3.1
Lung ca. NCI-H460	0.0	0.0	0.2	0.0
Lung ca. HOP-62	0.0	0.0	0.6	0.0
Lung ca. NCI-H522	0.0	0.0	2.4	1.4
Liver	0.0	0.0	0.1	0.0
Fetal Liver	0.0	0.0	0.6	0.5
Liver ca. HepG2	0.0	0.0	0.1	0.5
Kidney Pool	6.5	0.0	34.9	22.8
Fetal Kidney	0.0	0.0	5.1	2.4
Renal ca. 786-0	0.0	0.0	0.2	0.0
Renal ca. A498	0.0	0.0	0.1	0.0
Renal ca. ACHN	0.0	0.0	0.7	0.7
Renal ca. UO-31	0.0	0.0	0.3	0.0
Renal ca. TK-10	0.0	0.0	2.5	3.0
Bladder	0.0	0.0	3.0	3.4
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.1
Gastric ca. KATO III	0.0	0.0	0.4	0.0
Colon ca. SW-948	0.0	0.0	0.0	0.0
Colon ca. SW480	9.5	0.0	39.0	28.3

Colon ca.* (SW480 met) SW620	7.7	0.0	15.5	11.7
Colon ca. HT29	0.0	0.0	0.0	0.0
Colon ca. HCT-116	1.6	0.0	3.8	5.0
Colon ca. CaCo-2	10.4	0.0	22.2	14.9
Colon cancer tissue	0.0	0.0	6.5	9.2
Colon ca. SW1116	0.0	0.0	1.7	2.2
Colon ca. Colo-205	0.0	0.0	0.2	0.0
Colon ca. SW-48	0.0	0.0	1.3	1.4
Colon Pool	0.0	0.0	28.7	14.2
Small Intestine Pool	0.0	0.0	10.5	7.4
Stomach Pool	0.0	0.0	6.2	9.2
Bone Marrow Pool	0.0	0.0	11.3	4.6
Fetal Heart	0.0	0.0	24.3	11.3
Heart Pool	5.2	0.0	23.0	15.2
Lymph Node Pool	0.0	0.0	30.4	14.1
Fetal Skeletal Muscle	36.9	0.0	46.7	33.0
Skeletal Muscle Pool	12.3	0.0	21.5	21.2
Spleen Pool	0.0	0.0	2.0	1.2
Thymus Pool	0.0	0.0	7.5	6.1
CNS cancer (glio/astro) U87-MG	1.6	0.0	6.1	10.4
CNS cancer (glio/astro) U-118-MG	0.0	0.0	2.9	3.4
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	1.7	1.8
CNS cancer (astro) SF-539	0.0	0.0	0.2	0.0
CNS cancer (astro) SNB-75	1.9	0.0	5.9	12.0
CNS cancer (glio) SNB-19	84.1	25.0	**100.0**	**100.0**
CNS cancer (glio) SF-295	1.8	0.0	9.0	7.7

Brain (Amygdala) Pool	2.3	0.0	6.9	5.5
Brain (cerebellum)	6.6	0.0	11.1	11.0
Brain (fetal)	3.0	0.0	11.5	6.9
Brain (Hippocampus) Pool	3.1	0.0	11.0	8.5
Cerebral Cortex Pool	1.7	0.0	7.5	6.8
Brain (Substantia nigra) Pool	1.8	0.0	8.5	5.2
Brain (Thalamus) Pool	0.0	0.0	10.0	6.8
Brain (whole)	0.0	0.0	8.0	6.8
Spinal Cord Pool	3.2	0.0	12.8	6.4
Adrenal Gland	0.0	0.0	6.1	8.4
Pituitary gland Pool	0.0	0.0	0.8	0.6
Salivary Gland	0.0	0.0	1.1	1.6
Thyroid (female)	0.0	0.0	0.8	2.6
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.9
Pancreas Pool	0.0	0.0	1.1	0.8

Table AMG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6434, Run 268713326	Tissue Name	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6434, Run 268713326
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.0	0.0	HUVEC IL-11	0.0	0.0
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0

Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	3.9	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	0.0	Astrocytes rest	12.0	**100.0**
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	**100.0**	97.3
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	0.1	7.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	0.0	0.0	Liver cirrhosis	0.0	3.4
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.1	7.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0

Two Way MLR 3 day	0.0	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	0.2	72.7
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.1	36.6
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.1	62.4
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	0.1	52.5
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	14.6
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.2	41.5
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	5.1
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	7.2
EOL-1 dbcAMP	0.1	4.4	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	0.1	24.5
Dendritic cells none	0.0	4.5	Dermal fibroblast IL-4	0.1	28.7
Dendritic cells LPS	0.0	0.0	Dermal Fibroblasts rest	0.1	44.4
Dendritic cells anti-CD40	0.0	0.0	Neutrophils TNFa+LPS	0.0	0.0
Monocytes rest	0.0	0.0	Neutrophils rest	0.0	0.0
Monocytes LPS	0.0	5.9	Colon	0.0	4.1
Macrophages rest	0.0	0.0	Lung	0.0	0.0
Macrophages LPS	0.1	9.1	Thymus	0.0	0.0
HUVEC none	0.0	0.0	Kidney	0.1	8.1
HUVEC starved	0.0	0.0			

CNS_neurodegeneration_v1.0 Summary: Ag6430/Ag6434 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this

experiment. See Panel 1.6 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6424/Ag6430/Ag6434 Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, moderate to low levels of expression of this gene is also seen in some of the colon, ovarian and brain cancer cell lines. Thus, expression of this gene may be used as a marker to detect the presence of colon, ovarian and brain cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of these cancers. Moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. Moderate levels of expression of this gene is seen in normal tissues represented by breast, testis, prostate, uterus, gastrointestinal tract, and tissues with metabolic/endocrine functions including adipose, heart, skeletal muscle, and adernal gland. Therefore, therapeutic modulation of this gene or its protein product may be useful in the treatment of diseases associated with these tissues, including obesity, diabetes and inflammatory bowel disease. In addition, moderate to low levels of expression of this gene is also seen in some regions of central nervous system, and some brain, colon and ovarian cancer cell lines.

Panel 4.1D Summary: Ag6430/Ag6434 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.8). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AN. CG56054-05: Integrin alpha 7-like protein.

Expression of gene CG56054-05 was assessed using the primer-probe set Ag6436, described in Table ANA.

Table ANA. Probe Name Ag6436

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gggcaagattgttacctgtg-3'	20	402	471
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	440	472
Reverse	5'-ccctggatgcccatc-3'	15	466	473

AO. CG56054-06 and CG56054-07: Integrin alpha 7-like protein.

Expression of gene CG56054-06 and CG56054-07 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6431, Ag6438, Ag6439, Ag6440, Ag6413 and Ag6964, described in Tables AOA, AOB, AOC, AOD, AOE, AOF, AOG, AOH and AOI. Results of the RTQ-PCR runs are shown in Tables AOJ, AOK, AOL, AOM, AON and AOO. Note that CG56054-07 is recognized by probe-primer sets Ag6425 and Ag6440.

Table AOA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	1057	474
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	1079	475
Reverse	5'-aacagcagctctacctccagtt-3'	22	1113	476

Table AOB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	1496	477
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	1535	478
Reverse	5'-gcgcagtccagggtg-3'	15	1621	479

Table AOC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	2118	480
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	2150	481
Reverse	5'-gccctggatgcccat-3'	15	2169	482

Table AOD. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	1615	483
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	1656	484
Reverse	5'-ccgcgcggtcaaa-3'	13	1682	485

Table AOE. Probe Name Ag6438

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cagttgcagccctgga-3'	16	342	486
Probe	TET-5'-ccaggttccccgtgtgacgttc-3'-TAMRA	22	397	487
Reverse	5'-tcttccaggttacggctca-3'	19	420	488

Table AOF. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1872	489
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1892	490
Reverse	5'-gaagaatcccatcttccacag-3'	21	1958	491

Table AOG. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No

Forward	5'-accatcctgaggaacaactg-3'	20	2075	492
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	2142	493
Reverse	5'-ccctggatgcccatc-3'	15	2168	494

Table AOH. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	695	495
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	746	496
Reverse	5'-gctgttgttccatccacatc-3'	20	788	497

Table AOI. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	1701	498
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	1672	499
Reverse	5'-gccaactgtgtggtgttca-3'	19	1646	500

Table AOJ. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.8	21.6	18.9	19.2
AD 2 Hippo	41.2	52.9	28.7	28.9	61.1	49.7
AD 3 Hippo	8.9	6.4	7.5	6.1	9.7	20.4
AD 4 Hippo	14.8	25.5	18.8	17.6	23.3	5.6
AD 5 Hippo	44.8	41.8	38.4	42.6	34.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	90.1

Control 2 Hippo	24.3	36.1	29.5	32.5	29.9	28.5
Control 4 Hippo	42.9	43.8	32.3	37.9	54.7	86.5
Control (Path) 3 Hippo	14.2	11.4	6.0	6.4	5.8	0.0
AD 1 Temporal Ctx	23.3	15.9	17.1	24.5	12.6	16.8
AD 2 Temporal Ctx	41.5	47.3	39.8	27.5	59.0	21.6
AD 3 Temporal Ctx	9.5	9.8	11.3	9.0	17.1	5.7
AD 4 Temporal Ctx	30.6	39.0	25.3	30.4	29.9	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	36.3	41.8	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	32.3	38.7	39.2	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	46.7	47.6	48.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	50.3	50.3	17.0	59.9
Control 1 Temporal Ctx	12.2	23.0	15.6	24.0	23.3	46.7
Control 2 Temporal Ctx	14.2	32.5	17.4	14.9	43.5	50.0
Control 3 Temporal Ctx	15.1	15.3	14.5	16.5	9.2	9.5
Control 3 Temporal Ctx	23.7	25.0	13.1	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	30.6	39.8	51.1	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	20.4	24.8	7.2	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	10.9	11.9	9.9	31.0

Control (Path) 4 Temporal Ctx	21.9	27.4	18.2	21.6	14.9	39.5
AD 1 Occipital Ctx	16.0	11.9	11.5	16.0	5.8	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	8.8	10.2	7.8	4.9
AD 4 Occipital Ctx	18.9	23.7	17.9	18.6	35.4	11.1
AD 5 Occipital Ctx	24.8	28.3	22.5	22.7	16.6	42.3
AD 6 Occipital Ctx	20.6	31.9	17.0	22.1	23.5	14.8
Control 1 Occipital Ctx	9.5	14.4	8.7	7.2	15.2	8.8
Control 2 Occipital Ctx	31.9	42.6	33.2	29.3	35.8	82.4
Control 3 Occipital Ctx	18.8	13.0	17.1	19.2	4.4	8.8
Control 4 Occipital Ctx	18.2	17.0	12.6	13.6	12.9	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	36.1	39.5	22.4	**100.0**
Control (Path) 2 Occipital Ctx	9.6	14.1	7.9	7.0	5.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	6.0	5.9	6.7	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	10.2	11.4	11.9	32.8
Control 1 Parietal Ctx	14.4	21.9	16.3	15.7	33.2	9.2
Control 2 Parietal Ctx	32.8	28.9	28.3	37.1	17.4	28.1
Control 3 Parietal Ctx	20.6	19.8	8.7	10.8	21.6	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	39.2	37.9	47.3	69.3

Control (Path) 2 Parietal Ctx	22.1	23.8	22.5	18.7	17.1	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	7.1	12.0	11.7	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	8.8	27.9	29.3	27.5

Table AOK. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4

Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AOL. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5

Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AOM. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6438, Run 277223173	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	17.4	13.8	25.0	17.3	3.7	18.8
Melanoma * Hs688(A).T	0.5	0.0	0.8	0.9	0.0	0.4	0.0	0.7
Melanoma * Hs688(B).T	2.7	0.2	2.5	2.2	0.0	2.9	0.8	2.4
Melanoma * M14	0.3	0.0	0.4	0.4	0.0	0.4	0.0	0.7
Melanoma * LOXIMVI	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
Melanoma * SK-MEL-5	15.2	2.2	18.2	14.6	29.5	18.3	3.0	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.2	0.0	0.0	0.0	0.1
Testis Pool	5.2	3.5	10.4	9.0	4.6	9.1	3.0	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	1.9	1.8	0.0	1.3	1.2	4.3
Prostate Pool	8.1	1.0	11.3	12.1	7.7	28.5	2.1	10.0
Placenta	0.5	0.0	0.1	0.1	0.0	0.5	0.0	0.4
Uterus Pool	2.2	1.5	4.6	4.5	0.0	5.3	2.3	4.1
Ovarian ca. OVCAR-3	0.9	0.3	0.7	1.1	0.0	1.6	0.4	4.0
Ovarian ca. SK-OV-3	0.8	0.2	0.8	0.9	0.0	1.3	0.5	1.7

Ovarian ca. OVCAR-4	0.2	0.0	0.4	0.8	0.0	0.9	0.0	0.5
Ovarian ca. OVCAR-5	1.6	1.3	1.3	1.7	0.0	1.4	4.2	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	84.7	97.9	3.5	69.3	**100.0**	75.8
Ovarian ca. OVCAR-8	13.6	21.9	15.6	14.6	0.0	17.3	18.2	16.7
Ovary	2.7	0.3	3.1	2.3	0.8	2.8	0.8	2.4
Breast ca. MCF-7	0.3	0.0	0.1	0.2	0.0	0.5	0.3	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.2	0.2	0.0	0.2	0.0	0.3
Breast ca. BT 549	0.5	0.0	0.1	0.5	0.0	0.6	0.0	0.4
Breast ca. T47D	0.0	0.0	0.2	0.3	0.0	0.4	0.3	0.5
Breast ca. MDA-N	0.6	0.0	0.6	0.6	0.0	0.6	0.3	0.8
Breast Pool	15.0	4.1	14.6	10.7	21.9	12.2	3.5	16.7
Trachea	4.5	0.7	4.8	4.2	9.7	4.7	1.4	5.6
Lung	2.8	0.7	4.2	3.2	0.0	3.9	5.3	5.1
Fetal Lung	3.9	0.3	5.0	4.8	7.4	5.3	2.9	6.1
Lung ca. NCI-N417	2.0	0.9	3.3	2.6	0.0	4.0	2.0	2.3
Lung ca. LX-1	3.5	2.7	5.0	3.5	0.0	4.9	6.3	44.1
Lung ca. NCI-H146	0.1	0.0	0.1	0.2	0.0	0.1	0.0	0.1
Lung ca. SHP-77	4.0	0.4	5.3	4.5	0.0	4.5	0.8	3.8
Lung ca. A549	0.3	2.6	0.0	0.4	0.0	0.6	2.2	4.7

Lung ca. NCI-H526	0.2	0.0	0.6	0.3	0.0	0.4	0.3	0.5
Lung ca. NCI-H23	2.9	1.0	4.8	3.2	0.0	2.9	2.3	10.3
Lung ca. NCI-H460	0.0	0.0	0.1	0.3	0.0	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.0	1.0	0.6	0.0	0.5	0.0	0.7
Lung ca. NCI-H522	1.7	0.6	1.7	1.3	0.0	3.3	2.5	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	0.4	2.0
Fetal Liver	0.3	0.3	0.6	0.5	0.0	0.8	0.8	8.2
Liver ca. HepG2	0.1	0.3	0.0	0.2	0.0	0.1	0.9	2.4
Kidney Pool	27.9	0.0	33.9	28.1	**100.0**	43.2	14.6	32.8
Fetal Kidney	1.4	0.0	4.1	4.0	2.4	5.8	3.4	11.5
Renal ca. 786-0	0.2	0.0	0.3	0.1	0.0	0.3	0.0	0.9
Renal ca. A498	0.0	1.8	0.0	0.3	0.0	0.5	3.8	8.5
Renal ca. ACHN	1.5	0.5	1.7	1.5	0.9	1.2	0.5	2.5
Renal ca. UO-31	0.3	0.0	0.2	0.2	0.0	0.6	0.0	0.3
Renal ca. TK-10	1.9	0.4	2.0	1.9	0.0	2.1	0.5	4.6
Bladder	4.2	0.0	5.5	5.1	6.1	8.3	0.9	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.9	1.2	0.0	1.1	0.8	6.7
Gastric ca. KATO III	0.4	0.5	0.2	0.3	0.0	0.4	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.0	0.3	2.2	1.2
Colon ca. SW480	20.9	5.2	27.0	23.3	42.3	23.0	6.3	33.7

Colon ca.* (SW480 met) SW620	13.3	4.8	12.8	10.3	8.8	6.1	7.2	25.0
Colon ca. HT29	0.2	0.0	0.2	0.2	0.0	0.0	0.3	0.3
Colon ca. HCT-116	2.1	0.2	2.5	2.0	0.0	2.1	0.6	4.3
Colon ca. CaCo-2	15.0	3.6	19.1	16.7	31.4	18.3	6.5	38.2
Colon cancer tissue	9.0	3.3	11.9	7.6	6.3	7.7	4.4	20.4
Colon ca. SW1116	1.3	3.0	2.0	1.5	0.0	1.8	2.1	6.0
Colon ca. Colo-205	0.1	0.4	0.2	0.0	0.0	0.2	1.3	0.8
Colon ca. SW-48	0.8	3.6	1.5	1.5	0.0	1.4	3.0	2.6
Colon Pool	20.3	5.0	23.2	18.7	22.7	25.5	8.1	20.6
Small Intestine Pool	14.0	1.7	11.2	13.0	3.7	12.8	2.0	10.4
Stomach Pool	8.1	2.3	9.5	9.3	15.0	8.5	4.2	10.7
Bone Marrow Pool	6.8	1.6	10.2	8.7	7.1	18.7	3.5	12.5
Fetal Heart	10.1	2.3	24.5	21.8	44.4	33.7	8.6	20.7
Heart Pool	28.7	7.0	25.9	17.2	4.7	33.7	10.7	26.1
Lymph Node Pool	17.6	6.1	22.1	23.7	50.7	19.9	6.7	24.7
Fetal Skeletal Muscle	31.9	5.2	48.6	46.3	85.9	19.1	19.2	50.7
Skeletal Muscle Pool	17.4	9.2	29.5	25.9	26.1	22.1	22.7	32.3

Spleen Pool	0.9	0.0	2.0	1.7	0.0	2.7	0.6	3.1
Thymus Pool	4.4	2.0	8.1	9.4	16.3	7.7	3.1	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	10.7	10.0	2.9	10.9	2.2	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	3.8	3.1	0.0	3.8	0.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.1	1.0	0.0	1.4	0.5	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.1	0.2	0.0	0.1	0.2	0.1
CNS cancer (astro) SNB-75	8.1	1.1	6.5	10.0	0.0	11.7	2.8	9.7
CNS cancer (glio) SNB-19	79.6	79.0	**100.0**	**100.0**	9.1	**100.0**	97.9	**100.0**
CNS cancer (glio) SF-295	8.2	0.0	8.0	7.8	5.0	8.2	1.5	14.8
Brain (Amygdala) Pool	3.7	0.8	6.2	4.8	6.0	8.0	4.4	5.3
Brain (cerebellum)	12.0	0.4	10.7	9.7	11.8	8.8	1.2	9.7
Brain (fetal)	4.2	0.7	6.6	5.6	8.5	6.8	2.1	6.4

Brain (Hippocampus) Pool	7.5	3.2	8.6	6.9	4.3	11.0	4.3	10.2
Cerebral Cortex Pool	9.7	0.6	7.5	0.7	3.4	11.6	2.0	8.7
Brain (Substantia nigra) Pool	7.4	2.2	10.4	4.7	5.8	10.0	2.0	9.3
Brain (Thalamus) Pool	7.6	2.7	9.3	0.2	22.5	9.7	2.8	8.7
Brain (whole)	6.1	0.4	5.8	0.3	8.6	5.6	1.9	8.7
Spinal Cord Pool	10.1	2.3	11.0	7.6	27.4	12.2	4.2	9.0
Adrenal Gland	3.5	0.3	3.9	3.7	3.2	4.8	0.9	4.1
Pituitary gland Pool	0.9	0.0	1.2	1.1	0.0	1.4	0.6	0.5
Salivary Gland	0.9	0.0	1.3	0.9	0.0	1.1	0.0	1.0
Thyroid (female)	2.0	0.3	2.5	2.5	0.0	1.9	1.3	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.7	0.6	0.0	0.7	0.6	2.2
Pancreas Pool	1.2	0.0	1.1	1.6	0.0	3.2	1.0	2.3

Table AON. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	0.0	0.7	0.0
Secondary Th2 act	0.5	0.3	0.0	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0

Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.4	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.0
Primary Th1 rest	0.0	0.0	0.0	0.3	1.2
Primary Th2 rest	0.0	0.0	0.0	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.4	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	1.2
LAK cells rest	5.6	5.0	2.7	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	0.0	2.5	1.4
Two Way MLR 3 day	1.4	1.1	0.0	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.0	0.9	0.0
Two Way MLR 7 day	2.3	0.7	13.2	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	0.0	0.0

PBMC PHA-L	0.3	0.2	0.0	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	13.8	5.3	0.0
Dendritic cells LPS	1.6	0.3	0.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.2	0.0
Monocytes rest	0.2	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	1.8	2.6
Macrophages rest	0.9	1.8	0.0	0.6	0.0
Macrophages LPS	7.5	4.0	0.0	6.3	9.2
HUVEC none	0.1	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.0	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0

Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	1.5	0.0
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	74.2	74.7	95.9
KU-812 (Basophil) rest	0.1	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	6.7	8.5
NCI-H292 none	0.3	0.3	0.0	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	19.1	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	23.5	26.8	96.6

Lung fibroblast IL-13	31.6	14.6	4.5	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	8.5	20.2	26.6
Dermal fibroblast IL-4	10.7	14.6	4.1	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	8.0	46.7	47.3
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.0	9.5	8.4
Lung	2.2	1.2	0.0	4.6	2.1
Thymus	3.1	0.8	0.0	0.4	2.4
Kidney	4.2	4.4	4.9	9.7	5.2

Table AOO. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1

Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6431/Ag6439/Ag6440/Ag6442 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric,

colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

Summary: Ag6413/Ag6425/Ag6431/Ag6439/Ag6440/Ag6964 Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system,

tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6438 Highest expression is detected in kidney (CTs=32.9). In addition, low levels of expression also seen in fetal heart, lymph node, fetal and adult skeletal muscle, spinal cord and a couple of colon cancer cell lines.

Panel 4.1D Summary: Ag4983/Ag6413/Ag6425/Ag6431/Ag6439 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this

gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AP. CG56054-08: Integrin alpha 7-like protein.

Expression of gene CG56054-08 was assessed using the primer-probe sets Ag6424, Ag6425, Ag6426, Ag6430, Ag6439 and Ag6440, described in Tables APA, APB, APC, APD, APE and APF. Results of the RTQ-PCR runs are shown in Tables APG, APH and API.

Table APA. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	501
	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	502
Reverse	5'-aaaagcaacccctttccaa-3'	18	824	503

Table APB. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1592	504
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1624	505
Reverse	5'-gccctggatgcccat-3'	15	1643	506

Table APC. Probe Name Ag6426

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtcactgggctgggatct-3'	18	1249	507
Probe	TET-5'-ctctccggctctgcggctc-3'-TAMRA	19	1270	508
Reverse	5'-actccttctgccaccaca-3'	18	1347	509

Table APD. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	510
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	511
Reverse	5'-gggagccggtcagca-3'	15	899	512

Table APE. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1346	513
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1366	514
Reverse	5'-gaagaatcccatcttccacag-3'	21	1432	515

Table APF. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1549	516
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	1616	517
Reverse	5'-ccctggatgcccatc-3'	15	1642	518

Table APG. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003
AD 1 Hippo	20.0	21.6	18.9
AD 2 Hippo	48.0	28.9	61.1
AD 3 Hippo	11.6	6.1	9.7
AD 4 Hippo	17.1	17.6	23.3
AD 5 hippo	39.2	42.6	34.6
AD 6 Hippo	100.0	100.0	100.0

Control 2 Hippo	17.9	32.5	29.9
Control 4 Hippo	38.4	37.9	54.7
Control (Path) 3 Hippo	10.2	6.4	5.8
AD 1 Temporal Ctx	12.1	24.5	12.6
AD 2 Temporal Ctx	36.6	27.5	59.0
AD 3 Temporal Ctx	11.7	9.0	17.1
AD 4 Temporal Ctx	15.6	30.4	29.9
AD 5 Inf Temporal Ctx	43.8	41.8	41.8
AD 5 SupTemporal Ctx	56.6	38.7	39.2
AD 6 Inf Temporal Ctx	40.9	47.6	48.6
AD 6 Sup Temporal Ctx	44.1	50.3	17.0
Control 1 Temporal Ctx	11.9	24.0	23.3
Control 2 Temporal Ctx	16.7	14.9	43.5
Control 3 Temporal Ctx	13.0	16.5	9.2
Control 4 Temporal Ctx	18.9	23.8	30.1
Control (Path) 1 Temporal Ctx	32.5	39.8	51.1
Control (Path) 2 Temporal Ctx	19.5	24.8	7.2
Control (Path) 3 Temporal Ctx	12.9	11.9	9.9
Control (Path) 4 Temporal Ctx	19.8	21.6	14.9
AD 1 Occipital Ctx	16.2	16.0	5.8
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	11.7	10.2	7.8
AD 4 Occipital Ctx	12.6	18.6	35.4
AD 5 Occipital Ctx	16.7	22.7	16.6
AD 6 Occipital Ctx	17.8	22.1	23.5

Control 1 Occipital Ctx	11.3	7.2	15.2
Control 2 Occipital Ctx	24.8	29.3	35.8
Control 3 Occipital Ctx	16.4	19.2	4.4
Control 4 Occipital Ctx	12.1	13.6	12.9
Control (Path) 1 Occipital Ctx	32.8	39.5	22.4
Control (Path) 2 Occipital Ctx	9.6	7.0	5.0
Control (Path) 3 Occipital Ctx	8.4	5.9	6.7
Control (Path) 4 Occipital Ctx	15.9	11.4	11.9
Control 1 Parietal Ctx	15.2	15.7	33.2
Control 2 Parietal Ctx	39.5	37.1	17.4
Control 3 Parietal Ctx	14.5	10.8	21.6
Control (Path) 1 Parietal Ctx	33.4	37.9	47.3
Control (Path) 2 Parietal Ctx	20.0	18.7	17.1
Control (Path) 3 Parietal Ctx	15.0	12.0	11.7
Control (Path) 4 Parietal Ctx	28.3	27.9	29.3

Table APH. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	0.0	2.6	8.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.0	0.5	0.4	0.0
Melanoma* Hs688(B).T	0.0	0.2	0.6	2.9	0.8
Melanoma* M14	0.0	0.0	0.7	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0	0.0

Melanoma* SK-MEL-5	0.0	2.2	22.5	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.3	0.0	0.0
Testis Pool	0.0	3.5	4.2	9.1	3.0
Prostate ca.* (bone met) PC-3	0.0	0.5	1.0	1.3	1.2
Prostate Pool	0.0	1.0	8.5	28.5	2.1
Placenta	0.0	0.0	0.1	0.5	0.0
Uterus Pool	0.0	1.5	2.6	5.3	2.3
Ovarian ca. OVCAR-3	0.0	0.3	0.8	1.6	0.4
Ovarian ca. SK-OV-3	0.0	0.2	1.5	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.5	0.9	0.0
Ovarian ca. OVCAR-5	0.0	1.3	1.5	1.4	4.2
Ovarian ca. IGROV-1	**100.0**	**100.0**	90.8	69.3	**100.0**
Ovarian ca. OVCAR-8	5.6	21.9	11.9	17.3	18.2
Ovary	0.0	0.3	2.1	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.4	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.3	0.6	0.0
Breast ca. T47D	0.0	0.0	0.3	0.4	0.3
Breast ca. MDA-N	0.0	0.0	0.7	0.6	0.3
Breast Pool	0.0	4.1	19.5	12.2	3.5
Trachea	0.0	0.7	2.9	4.7	1.4
Lung	0.0	0.7	1.3	3.9	5.3
Fetal Lung	0.0	0.3	4.0	5.3	2.9
Lung ca. NCI-N417	2.0	0.9	2.7	4.0	2.0
Lung ca. LX-1	3.1	2.7	7.0	4.9	6.3

Lung ca. NCI-H146	0.0	0.0	0.5	0.1	0.0
Lung ca. SHP-77	2.3	0.4	6.3	4.5	0.8
Lung ca. A549	0.0	2.6	0.3	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.7	0.4	0.3
Lung ca. NCI-H23	0.0	1.0	4.5	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.6	0.5	0.0
Lung ca. NCI-H522	0.0	0.6	2.4	3.3	2.5
Liver	0.0	0.0	0.1	0.1	0.4
Fetal Liver	0.0	0.3	0.6	0.8	0.8
Liver ca. HepG2	0.0	0.3	0.1	0.1	0.9
Kidney Pool	6.5	0.0	34.9	43.2	14.6
Fetal Kidney	0.0	0.0	5.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.2	0.3	0.0
Renal ca. A498	0.0	1.8	0.1	0.5	3.8
Renal ca. ACHN	0.0	0.5	0.7	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.3	0.6	0.0
Renal ca. TK-10	0.0	0.4	2.5	2.1	0.5
Bladder	0.0	0.0	3.0	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.1	0.8
Gastric ca. KATO III	0.0	0.5	0.4	0.4	0.4
Colon ca. SW-948	0.0	1.5	0.0	0.3	2.2
Colon ca. SW480	9.5	5.2	39.0	23.0	6.3
Colon ca.* (SW480 met) SW620	7.7	4.8	15.5	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.0	0.3
Colon ca. HCT-116	1.6	0.2	3.8	2.1	0.6
Colon ca. CaCo-2	10.4	3.6	22.2	18.3	6.5
Colon cancer tissue	0.0	3.3	6.5	7.7	4.4
Colon ca. SW1116	0.0	3.0	1.7	1.8	2.1
Colon ca. Colo-205	0.0	0.4	0.2	0.2	1.3

Colon ca. SW-48	0.0	3.6	1.3	1.4	3.0
Colon Pool	0.0	5.0	28.7	25.5	8.1
Small Intestine Pool	0.0	1.7	10.5	12.8	2.0
Stomach Pool	0.0	2.3	6.2	8.5	4.2
Bone Marrow Pool	0.0	1.6	11.3	18.7	3.5
Fetal Heart	0.0	2.3	24.3	33.7	8.6
Heart Pool	5.2	7.0	23.0	33.7	10.7
Lymph Node Pool	0.0	6.1	30.4	19.9	6.7
Fetal Skeletal Muscle	36.9	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	12.3	9.2	21.5	22.1	22.7
Spleen Pool	0.0	0.0	2.0	2.7	0.6
Thymus Pool	0.0	2.0	7.5	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.6	1.5	6.1	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.0	0.3	2.9	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	1.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.9	1.1	5.9	11.7	2.8
CNS cancer (glio) SNB-19	84.1	79.0	**100.0**	**100.0**	97.9
CNS cancer (glio) SF-295	1.8	0.0	9.0	8.2	1.5
Brain (Amygdala) Pool	2.3	0.8	6.9	8.0	4.4
Brain (cerebellum)	6.6	0.4	11.1	8.8	1.2
Brain (fetal)	3.0	0.7	11.5	6.8	2.1
Brain (Hippocampus) Pool	3.1	3.2	11.0	11.0	4.3
Cerebral Cortex Pool	1.7	0.6	7.5	11.6	2.0

Brain (Substantia nigra) Pool	1.8	2.2	8.5	10.0	2.0
Brain (Thalamus) Pool	0.0	2.7	10.0	9.7	2.8
Brain (whole)	0.0	0.4	8.0	5.6	1.9
Spinal Cord Pool	3.2	2.3	12.8	12.2	4.2
Adrenal Gland	0.0	0.3	6.1	4.8	0.9
Pituitary gland Pool	0.0	0.0	0.8	1.4	0.6
Salivary Gland	0.0	0.0	1.1	1.1	0.0
Thyroid (female)	0.0	0.3	0.8	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.7	0.6
Pancreas Pool	0.0	0.0	1.1	3.2	1.0

Table API. Panel 4.1D

Tissue Name	**Rel. Exp.(%) Ag6425, Run 268713999**	**Rel. Exp.(%) Ag6430, Run 268767563**	**Rel. Exp.(%) Ag6439, Run 268760823**
Secondary Th1 act	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2
Primary Th2 rest	0.0	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	2.6
CD45RO CD4 lymphocyte act	0.0	0.0	2.3

CD8 lymphocyte act	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2
LAK cells rest	2.7	0.1	15.2
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	0.1	9.0
NK Cells IL-2 rest	0.0	0.0	1.4
Two Way MLR 3 day	0.0	0.0	1.4
Two Way MLR 5 day	0.0	0.0	0.0
Two Way MLR 7 day	13.2	0.0	3.7
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.1	68.8
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	1.8
Dendritic cells none	13.8	0.0	0.0
Dendritic cells LPS	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	0.0	0.0
Monocytes rest	0.0	0.0	0.0

Monocytes LPS	0.0	0.0	2.6
Macrophages rest	0.0	0.0	0.0
Macrophages LPS	0.0	0.1	9.2
HUVEC none	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0
Astrocytes rest	**100.0**	12.0	**100.0**
Astrocytes TNFalpha + IL-1beta	74.2	**100.0**	95.9
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0

Liver cirrhosis	4.6	0.0	8.5
NCI-H292 none	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	0.2	94.0
Lung fibroblast TNF alpha + IL-1 beta	22.2	0.1	62.9
Lung fibroblast IL-4	19.1	0.1	34.9
Lung fibroblast IL-9	23.5	0.1	96.6
Lung fibroblast IL-13	4.5	0.0	13.4
Lung fibroblast IFN gamma	15.7	0.2	89.5
Dermal fibroblast CCD1070 rest	0.0	0.0	4.1
Dermal fibroblast CCD1070 TNF alpha	0.0	0.0	2.3
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0	0.0
Dermal fibroblast IFN gamma	8.5	0.1	26.6
Dermal fibroblast IL-4	4.1	0.1	25.5
Dermal Fibroblasts rest	8.0	0.1	47.3
Neutrophils TNFa+LPS	0.0	0.0	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	0.0	8.4
Lung	0.0	0.0	2.1
Thymus	0.0	0.0	2.4
Kidney	4.9	0.1	5.2

CNS_neurodegeneration_v1.0 Summary: Ag6430/Ag6439/Ag6440 Four experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of

individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6

Summary: Ag6424/Ag6425/Ag6430/Ag6439/Ag6440 Five experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary: Ag6425/Ag6430/Ag6439 Three experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AQ. CG56054-09: Integrin alpha 7-like protein.

Expression of gene CG56054-09 was assessed using the primer-probe sets Ag6425, Ag6435, Ag6437, Ag6439 and Ag6440, described in Tables AQA, AQB, AQC, AQD and AQE. Results of the RTQ-PCR runs are shown in Tables AQF, AQG and AQH.

Table AQA. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1240	519
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1272	520
Reverse	5'-gccctggatgcccat-3'	15	1291	521

Table AQB. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	522
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	523
Reverse	5'-cagggaccgggatga-3'	15	829	524

Table AQC. Probe Name Ag6437

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	525
Probe	TET-5'-cgcctcatcccggtccct-3'-TAMRA	18	825	526
Reverse	5'-ctcctccagaaaggtgctgt-3'	20	847	527

Table AQD. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	994	528
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1014	529
Reverse	5'-gaagaatcccatcttccacag-3'	21	1080	530

Table AQE. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1197	531

Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	1264	532
Reverse	5'-ccctggatgcccatc-3'	15	1290	533

Table AQF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003
AD 1 Hippo	17.1	21.6	18.9
AD 2 Hippo	27.9	28.9	61.1
AD 3 Hippo	4.8	6.1	9.7
AD 4 Hippo	18.3	17.6	23.3
AD 5 Hippo	46.7	42.6	34.6
AD 6 Hippo	**100.0**	**100.0**	**100.0**
Control 2 Hippo	8.5	32.5	29.9
Control 4 Hippo	29.9	37.9	54.7
Control (Path) 3 Hippo	5.2	6.4	5.8
AD 1 Temporal Ctx	12.8	24.5	12.6
AD 2 Temporal Ctx	45.1	27.5	59.0
AD 3 Temporal Ctx	4.1	9.0	17.1
AD 4 Temporal Ctx	6.8	30.4	29.9
AD 5 Inf Temporal Ctx	1.6	41.8	41.8
AD 5 Sup Temporal Ctx	33.2	38.7	39.2
AD 6 Inf Temporal Ctx	52.1	47.6	48.6
AD 6 Sup Temporal Ctx	37.6	50.3	17.0
Control 1 Temporal Ctx	6.7	24.0	23.3
Control 2 Temporal Ctx	7.3	14.9	43.5
Control 3 Temporal Ctx	4.4	16.5	9.2
Control 3 Temporal Ctx	11.7	23.8	30.1

Control (Path) 1 Temporal Ctx	24.8	39.8	51.1
Control (Path) 2 Temporal Ctx	9.8	24.8	7.2
Control (Path) 3 Temporal Ctx	3.5	11.9	9.9
Control (Path) 4 Temporal Ctx	14.8	21.6	14.9
AD 1 Occipital Ctx	15.0	16.0	5.8
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	8.0	10.2	7.8
AD 4 Occipital Ctx	6.8	18.6	35.4
AD 5 Occipital Ctx	12.7	22.7	16.6
AD 6 Occipital Ctx	5.9	22.1	23.5
Control 1 Occipital Ctx	4.1	7.2	15.2
Control 2 Occipital Ctx	20.3	29.3	35.8
Control 3 Occipital Ctx	7.5	19.2	4.4
Control 4 Occipital Ctx	3.3	13.6	12.9
Control (Path) 1 Occipital Ctx	25.9	39.5	22.4
Control (Path) 2 Occipital Ctx	7.4	7.0	5.0
Control (Path) 3 Occipital Ctx	2.3	5.9	6.7
Control (Path) 4 Occipital Ctx	21.0	11.4	11.9
Control 1 Parietal Ctx	12.5	15.7	33.2
Control 2 Parietal Ctx	41.2	37.1	17.4
Control 3 Parietal Ctx	13.2	10.8	21.6
Control (Path) 1 Parietal Ctx	22.5	37.9	47.3
Control (Path) 2 Parietal Ctx	26.8	18.7	17.1
Control (Path) 3 Parietal Ctx	7.5	12.0	11.7

Control (Path) 4 Parietal Ctx	20.6	27.9	29.3

Table AQG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	2.6	13.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.9	0.4	0.0
Melanoma* Hs688(B).T	0.2	1.9	2.9	0.8
Melanoma* M14	0.0	0.0	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	2.2	4.4	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.0
Testis Pool	3.5	10.0	9.1	3.0
Prostate ca.* (bone met) PC-3	0.5	1.8	1.3	1.2
Prostate Pool	1.0	10.0	28.5	2.1
Placenta	0.0	0.3	0.5	0.0
Uterus Pool	1.5	16.2	5.3	2.3
Ovarian ca. OVCAR-3	0.3	0.4	1.6	0.4
Ovarian ca. SK-OV-3	0.2	0.9	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.0
Ovarian ca. OVCAR-5	1.3	0.3	1.4	4.2
Ovarian ca. IGROV-1	**100.0**	27.0	69.3	**100.0**
Ovarian ca. OVCAR-8	21.9	7.6	17.3	18.2
Ovary	0.3	4.5	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.6	0.0
Breast ca. T47D	0.0	0.0	0.4	0.3

Breast ca. MDA-N	0.0	0.7	0.6	0.3
Breast Pool	4.1	42.9	12.2	3.5
Trachea	0.7	8.3	4.7	1.4
Lung	0.7	3.9	3.9	5.3
Fetal Lung	0.3	8.0	5.3	2.9
Lung ca. NCI-N417	0.9	0.2	4.0	2.0
Lung ca. LX-1	2.7	0.9	4.9	6.3
Lung ca. NCI-H146	0.0	0.0	0.1	0.0
Lung ca. SHP-77	0.4	0.2	4.5	0.8
Lung ca. A549	2.6	0.0	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.4	0.3
Lung ca. NCI-H23	1.0	0.6	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.5	0.0
Lung ca. NCI-H522	0.6	0.0	3.3	2.5
Liver	0.0	0.0	0.1	0.4
Fetal Liver	0.3	0.3	0.8	0.8
Liver ca. HepG2	0.3	0.0	0.1	0.9
Kidney Pool	0.0	100.0	43.2	14.6
Fetal Kidney	0.0	12.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.3	0.0
Renal ca. A498	1.8	0.0	0.5	3.8
Renal ca. ACHN	0.5	0.0	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.6	0.0
Renal ca. TK-10	0.4	0.7	2.1	0.5
Bladder	0.0	6.6	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.1	0.8
Gastric ca. KATO III	0.5	0.3	0.4	0.4
Colon ca. SW-948	1.5	0.0	0.3	2.2
Colon ca. SW480	5.2	4.4	23.0	6.3

Colon ca.* (SW480 met) SW620	4.8	1.7	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.3
Colon ca. HCT-116	0.2	0.5	2.1	0.6
Colon ca. CaCo-2	3.6	7.6	18.3	6.5
Colon cancer tissue	3.3	5.6	7.7	4.4
Colon ca. SW1116	3.0	1.1	1.8	2.1
Colon ca. Colo-205	0.4	0.0	0.2	1.3
Colon ca. SW-48	3.6	0.0	1.4	3.0
Colon Pool	5.0	44.8	25.5	8.1
Small Intestine Pool	1.7	26.8	12.8	2.0
Stomach Pool	2.3	24.0	8.5	4.2
Bone Marrow Pool	1.6	25.9	18.7	3.5
Fetal Heart	2.3	31.6	33.7	8.6
Heart Pool	7.0	23.5	33.7	10.7
Lymph Node Pool	6.1	64.6	19.9	6.7
Fetal Skeletal Muscle	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	9.2	24.7	22.1	22.7
Spleen Pool	0.0	2.4	2.7	0.6
Thymus Pool	2.0	18.4	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.5	5.8	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.3	1.5	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.1	3.1	11.7	2.8
CNS cancer (glio) SNB-19	79.0	12.8	**100.0**	97.9
CNS cancer (glio) SF-295	0.0	0.0	8.2	1.5

Brain (Amygdala) Pool	0.8	7.9	8.0	4.4
Brain (cerebellum)	0.4	1.8	8.8	1.2
Brain (fetal)	0.7	8.4	6.8	2.1
Brain (Hippocampus) Pool	3.2	9.9	11.0	4.3
Cerebral Cortex Pool	0.6	1.8	11.6	2.0
Brain (Substantia nigra) Pool	2.2	4.2	10.0	2.0
Brain (Thalamus) Pool	2.7	9.1	9.7	2.8
Brain (whole)	0.4	3.3	5.6	1.9
Spinal Cord Pool	2.3	13.1	12.2	4.2
Adrenal Gland	0.3	7.4	4.8	0.9
Pituitary gland Pool	0.0	1.8	1.4	0.6
Salivary Gland	0.0	2.3	1.1	0.0
Thyroid (female)	0.3	3.3	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.5	0.7	0.6
Pancreas Pool	0.0	3.5	3.2	1.0

Table AQH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0
Secondary Tr1 rest	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0
Primary Tr1 act	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2
Primary Th2 rest	0.0	0.0	0.0

Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	2.6
CD45RO CD4 lymphocyte act	0.0	1.6	2.3
CD8 lymphocyte act	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2
LAK cells rest	2.7	6.1	15.2
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	6.1	9.0
NK Cells IL-2 rest	0.0	0.0	1.4
Two Way MLR 3 day	0.0	0.9	1.4
Two Way MLR 5 day	0.0	0.0	0.0
Two Way MLR 7 day	13.2	2.9	3.7
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.0	68.8
EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	1.8
Dendritic cells none	13.8	0.7	0.0

Dendritic cells LPS	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	1.6	0.0
Monocytes rest	0.0	0.0	0.0
Monocytes LPS	0.0	0.0	2.6
Macrophages rest	0.0	0.0	0.0
Macrophages LPS	0.0	0.8	9.2
HUVEC none	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.5	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0
Astrocytes rest	**100.0**	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	74.2	97.9	95.9
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
Liver cirrhosis	4.6	5.1	8.5
NCI-H292 none	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	62.9	94.0
Lung fibroblast TNF alpha + IL-1 beta	22.2	25.2	62.9
Lung fibroblast IL-4	19.1	23.3	34.9
Lung fibroblast IL-9	23.5	20.4	96.6
Lung fibroblast IL-13	4.5	15.0	13.4
Lung fibroblast IFN gamma	15.7	29.9	89.5
Dermal fibroblast CCD1070 rest	0.0	5.6	4.1
Dermal fibroblast CCD1070 TNF alpha	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	0.0
Dermal fibroblast IFN gamma	8.5	20.0	26.6
Dermal fibroblast IL-4	4.1	22.7	25.5
Dermal Fibroblasts rest	8.0	20.7	47.3
Neutrophils TNFa+LPS	0.0	1.2	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	7.9	8.4
Lung	0.0	1.6	2.1
Thymus	0.0	2.0	2.4
Kidney	4.9	10.2	5.2

CNS_neurodegeneration_v1.0 Summary: Ag6435/Ag6439/Ag6440 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of the of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6425/ Ag6435/Ag6439/Ag6440 Highest expression of this gene is detected in kidney, ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=28-31). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary:: Ag6425/ Ag6435/Ag6439 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AR. CG56054-10 and CG56054-11:Integrin alpha 7-like protein.

Expression of gene CG56054-10 and CG56054-11 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6428, Ag6431, Ag6433, Ag6435, Ag6440, Ag6446, Ag6447, Ag6413 and Ag6964, described in Tables ARA, ARB, ARC, ARD, ARE, ARF, ARG, ARH, ARI, ARJ, ARK and ARL. Results of the RTQ-PCR runs are shown in Tables ARM, ARN, ARO, ARP, ARQ and ARR. Note Ag6433 is specific for CG56054-11.

Also, the CG56054-11 gene is only recognized by probe-primer sets Ag6433, Ag6431, Ag6446 and Ag6964.

Table ARA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	534
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	535
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	536

Table ARB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	537
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	538
Reverse	5'-gcgcagtccagggtg-3'	15	2906	539

Table ARC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3516	540
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3548	541
Reverse	5'-gccctggatgcccat-3'	15	3567	542

Table ARD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	543
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	544

Reverse	5'-agggagtagccgaagctct-3'	19	1378	545

Table ARE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	546
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	547
Reverse	5'-ccgcgcggtcaaa-3'	13	2967	548

Table ARF. Probe Name Ag6433

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggagtcagtgtcctctgctga-3'	21	534	549
Probe	TET-5'-ctgcccactctacagctttgaccgc-3'-TAMRA	25	615	550
Reverse	5'-cccagacatgcagcacag-3'	18	644	551

Table ARG. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	552
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	553
Reverse	5'-cagggaccgggatga-3'	15	829	554

Table ARH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	3473	555
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	3540	556
Reverse	5'-ccctggatgcccatc-3'	15	3566	557

Table ARI. Probe Name Ag6446

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcttcttccatcggagca-3'	18	3256	558
Probe	TET-5'-caactatcaccgggcctgtctggc-3'-TAMRA	24	3296	559
Reverse	5'-catggctgaaggctgca-3'	17	3322	560

Table ARJ. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	561
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	562
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	563

Table ARK. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	564
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	565
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	566

Table ARL. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	567
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	568
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	569

Table ARM. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6433, Run 268030711	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6446, Run 269254006	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	18.0	18.8	27.0	17.1	18.9	19.2	42.9	18.8
AD 2 Hippo	41.2	52.9	32.3	28.7	43.5	27.9	61.1	49.7	41.8	10.4
AD 3 Hippo	8.9	6.4	3.7	7.5	9.9	4.8	9.7	20.4	23.7	0.0
AD 4 Hippo	14.8	25.5	10.7	18.8	18.2	18.3	23.3	5.6	29.9	4.6
AD 5 Hippo	44.8	41.8	53.2	38.4	44.8	46.7	34.6	57.4	67.8	11.0
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1	**100.0**	**100.0**
Control 2 Hippo	24.3	36.1	18.7	29.5	20.7	8.5	29.9	28.5	39.2	3.1
Control 4 Hippo	42.9	43.8	27.0	32.3	52.1	29.9	54.7	86.5	62.4	43.8
Control (Path) 3 Hippo	14.2	11.4	4.6	6.0	6.8	5.2	5.8	0.0	14.6	5.3
AD 1 Temporal Ctx	23.3	15.9	12.9	17.1	23.7	12.8	12.6	16.8	72.7	9.0
AD 2 Temporal Ctx	41.5	47.3	31.0	39.8	24.7	45.1	59.0	21.6	43.2	21.0
AD 3 Temporal Ctx	9.5	9.8	6.0	11.3	11.5	4.1	17.1	5.7	36.3	3.9
AD 4 Temporal Ctx	30.6	39.0	20.2	25.3	19.1	6.8	29.9	8.7	43.2	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	36.3	30.6	1.6	41.8	73.7	63.3	23.7

AD 5 Sup Temporal Ctx	51.1	39.0	42.0	32.3	38.7	33.2	39.2	55.9	95.3	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	46.7	43.5	52.1	48.6	76.8	45.1	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	50.3	62.0	37.6	17.0	59.9	30.6	61.1
Control 1 Temporal Ctx	12.2	23.0	12.9	15.6	11.8	6.7	23.3	46.7	5.9	2.8
Control 2 Temporal Ctx	14.2	32.5	18.2	17.4	31.0	7.3	43.5	50.0	13.6	16.0
Control 3 Temporal Ctx	15.1	15.3	9.6	14.5	12.6	4.4	9.2	9.5	12.5	3.1
Control 3 Temporal Ctx	23.7	25.0	15.2	13.1	17.7	11.7	30.1	13.6	26.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	30.6	39.2	24.8	51.1	46.0	21.2	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	20.4	14.2	9.8	7.2	0.0	27.2	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	10.9	13.6	3.5	9.9	31.0	24.5	6.3
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	18.2	11.9	14.8	14.9	39.5	19.2	7.0

AD 1 Occipital Ctx	16.0	11.9	10.2	11.5	13.1	15.0	5.8	6.3	39.5	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	8.8	8.0	8.0	7.8	4.9	19.3	0.0
AD 4 Occipital Ctx	18.9	23.7	13.0	17.9	15.9	6.8	35.4	11.1	25.3	3.5
AD 5 Occipital Ctx	24.8	28.3	25.3	22.5	36.6	12.7	16.6	42.3	25.2	3.8
AD 6 Occipital Ctx	20.6	31.9	20.2	17.0	16.0	5.9	23.5	14.8	9.7	8.5
Control 1 Occipital Ctx	9.5	14.4	6.0	8.7	15.1	4.1	15.2	8.8	6.5	1.3
Control 2 Occipital Ctx	31.9	42.6	26.4	33.2	25.0	20.3	35.8	82.4	8.1	13.7
Control 3 Occipital Ctx	18.8	13.0	10.7	17.1	12.1	7.5	4.4	8.8	15.8	5.0
Control 4 Occipital Ctx	18.2	17.0	12.0	12.6	14.4	3.3	12.9	24.0	23.3	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	36.1	40.9	25.9	22.4	**100.0**	23.3	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	7.9	6.3	7.4	5.0	9.3	15.6	13.2

Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	6.0	5.3	2.3	6.7	4.1	4.5	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	10.2	5.8	21.0	11.9	32.8	5.9	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	16.3	13.2	12.5	33.2	9.2	5.7	5.0
Control 2 Parietal Ctx	32.8	28.9	34.4	28.3	27.4	41.2	17.4	28.1	74.2	25.5
Control 3 Parietal Ctx	20.6	19.8	11.5	8.7	18.2	13.2	21.6	9.1	8.6	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	39.2	44.1	22.5	47.3	69.3	24.0	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	22.5	16.5	26.8	17.1	37.6	23.7	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	7.1	8.7	7.5	11.7	10.4	11.0	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	8.8	14.0	20.6	29.3	27.5	27.0	9.4

Table ARN. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0

Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2

Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ARO. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1

Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4

Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ARP. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6433, Run 277222449	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6446, Run 277250179	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	20.0	17.4	13.8	19.5	13.2	3.7	1.7	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.8	0.9	0.3	0.9	0.0	0.1	0.7
Melanoma* Hs688(B).T	2.7	0.2	4.1	2.5	2.2	2.5	1.9	0.8	0.1	2.4
Melanoma* M14	0.3	0.0	0.7	0.4	0.4	0.5	0.0	0.0	0.1	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.1	0.1
Melanoma* SK-MEL-5	15.2	2.2	30.4	18.2	14.6	13.1	4.4	3.0	6.8	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.1	0.2	0.1	0.0	0.0	0.0	0.1
Testis Pool	5.2	3.5	8.8	10.4	9.0	10.4	10.0	3.0	5.8	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	2.5	1.9	1.8	1.5	1.8	1.2	7.7	4.3
Prostate Pool	8.1	1.0	11.5	11.3	12.1	15.0	10.0	2.1	1.9	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.5	0.3	0.0	0.9	0.4
Uterus Pool	2.2	1.5	4.5	4.6	4.5	4.7	16.2	2.3	0.3	4.1

Ovarian ca. OVCAR-3	0.9	0.3	1.1	0.7	1.1	0.9	0.4	0.4	4.8	4.0
Ovarian ca. SK-OV-3	0.8	0.2	1.7	0.8	0.9	1.2	0.9	0.5	2.5	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.4	0.8	0.3	0.0	0.0	0.5	0.5
Ovarian ca. OVCAR-5	1.6	1.3	2.9	1.3	1.7	2.1	0.3	4.2	15.6	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	77.9	84.7	97.9	**100.0**	27.0	**100.0**	5.4	75.8
Ovarian ca. OVCAR-8	13.6	21.9	14.0	15.6	14.6	17.1	7.6	18.2	4.2	16.7
Ovary	2.7	0.3	5.2	3.1	2.3	4.1	4.5	0.8	0.2	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.1	0.2	0.1	0.0	0.3	0.9	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.4	0.2	0.2	0.1	0.0	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.1	0.5	0.6	0.0	0.0	0.2	0.4
Breast ca. T47D	0.0	0.0	0.5	0.2	0.3	0.4	0.0	0.3	0.7	0.5
Breast ca. MDA-N	0.6	0.0	0.7	0.6	0.6	1.0	0.7	0.3	0.0	0.8
Breast Pool	15.0	4.1	21.8	14.6	10.7	15.5	42.9	3.5	2.0	16.7
Trachea	4.5	0.7	8.4	4.8	4.2	4.6	8.3	1.4	0.5	5.6
Lung	2.8	0.7	2.3	4.2	3.2	5.2	3.9	5.3	0.5	5.1

Fetal Lung	3.9	0.3	9.1	5.0	4.8	5.1	8.0	2.9	0.5	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	3.3	2.6	2.3	0.2	2.0	0.4	2.3
Lung ca. LX-1	3.5	2.7	6.5	5.0	3.5	4.1	0.9	6.3	**100.0**	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.1	0.2	0.3	0.0	0.0	0.1	0.1
Lung ca. SHP-77	4.0	0.4	6.8	5.3	4.5	6.1	0.2	0.8	0.1	3.8
Lung ca. A549	0.3	2.6	0.9	0.0	0.4	0.7	0.0	2.2	14.3	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.6	0.3	0.6	0.0	0.3	0.0	0.5
Lung ca. NCI-H23	2.9	1.0	4.6	4.8	3.2	3.3	0.6	2.3	15.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.1	0.3	0.0	0.0	0.0	0.1	0.3
Lung ca. HOP-62	0.5	0.0	0.5	1.0	0.6	0.6	0.0	0.0	0.2	0.7
Lung ca. NCI-H522	1.7	0.6	2.3	1.7	1.3	1.4	0.0	2.5	27.7	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.4	5.3	2.0
Fetal Liver	0.3	0.3	1.1	0.6	0.5	0.2	0.3	0.8	23.0	8.2
Liver ca. HepG2	0.1	0.3	0.2	0.0	0.2	0.3	0.0	0.9	7.3	2.4
Kidney Pool	27.9	0.0	47.0	33.9	28.1	28.3	**100.0**	14.6	5.3	32.8
Fetal Kidney	1.4	0.0	4.9	4.1	4.0	4.1	12.1	3.4	20.2	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.3	0.1	0.5	0.0	0.0	1.7	0.9
Renal ca. A498	0.0	1.8	0.2	0.0	0.3	0.0	0.0	3.8	23.0	8.5

Renal ca. ACHN	1.5	0.5	2.5	1.7	1.5	2.1	0.0	0.5	3.8	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.2	0.2	0.4	0.0	0.0	0.7	0.3
Renal ca. TK-10	1.9	0.4	3.1	2.0	1.9	2.9	0.7	0.5	6.4	4.6
Bladder	4.2	0.0	5.9	5.5	5.1	4.2	6.6	0.9	3.2	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	0.9	1.2	1.3	0.0	0.8	17.8	6.7
Gastric ca. KATO III	0.4	0.5	0.8	0.2	0.3	0.2	0.3	0.4	1.3	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.2	0.0	0.0	2.2	6.1	1.2
Colon ca. SW480	20.9	5.2	41.8	27.0	23.3	26.8	4.4	6.3	39.0	33.7
Colon ca.* (SW480 met) SW620	13.3	4.8	16.4	12.8	10.3	13.0	1.7	7.2	71.2	25.0
Colon ca. HT29	0.2	0.0	0.0	0.2	0.2	0.1	0.0	0.3	3.5	0.3
Colon ca. HCT-116	2.1	0.2	3.2	2.5	2.0	2.3	0.5	0.6	6.4	4.3
Colon ca. CaCo-2	15.0	3.6	27.0	19.1	16.7	16.5	7.6	6.5	78.5	38.2
Colon cancer tissue	9.0	3.3	11.0	11.9	7.6	10.0	5.6	4.4	21.9	20.4
Colon ca. SW1116	1.3	3.0	2.5	2.0	1.5	1.1	1.1	2.1	19.5	6.0
Colon ca. Colo-205	0.1	0.4	0.3	0.2	0.0	0.0	0.0	1.3	3.0	0.8
Colon ca. SW-48	0.8	3.6	1.4	1.5	1.5	1.0	0.0	3.0	4.2	2.6
Colon Pool	20.3	5.0	28.1	23.2	18.7	18.7	44.8	8.1	3.1	20.6

Small Intestine Pool	14.0	1.7	17.1	11.2	13.0	11.4	26.8	2.0	2.5	10.4
Stomach Pool	8.1	2.3	14.3	9.5	9.3	9.5	24.0	4.2	1.1	10.7
Bone Marrow Pool	6.8	1.6	14.3	10.2	8.7	16.6	25.9	3.5	1.1	12.5
Fetal Heart	10.1	2.3	25.5	24.5	21.8	21.6	31.6	8.6	2.7	20.7
Heart Pool	28.7	7.0	29.7	25.9	17.2	29.7	23.5	10.7	3.4	26.1
Lymph Node Pool	17.6	6.1	33.7	22.1	23.7	23.0	64.6	6.7	2.8	24.7
Fetal Skeletal Muscle	31.9	5.2	54.3	48.6	46.3	47.0	46.7	19.2	57.0	50.7
Skeletal Muscle Pool	17.4	9.2	29.3	29.5	25.9	34.2	24.7	22.7	24.3	32.3
Spleen Pool	0.9	0.0	1.9	2.0	1.7	1.4	2.4	0.6	2.6	3.1
Thymus Pool	4.4	2.0	10.4	8.1	9.4	8.8	18.4	3.1	1.4	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	14.9	10.7	10.0	13.2	5.8	2.2	6.3	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	4.7	3.8	3.1	3.8	1.5	0.8	5.1	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	2.1	1.0	2.0	0.7	0.5	3.9	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.1	0.2	0.2	0.2	0.2	0.3	0.1

CNS cancer (astro) SNB-75	8.1	1.1	14.9	6.5	10.0	11.4	3.1	2.8	2.4	9.7
CNS cancer (glio) SNB-19	79.6	79.0	**100.0**	**100.0**	**100.0**	98.6	12.8	97.9	5.2	**100.0**
CNS cancer (glio) SF-295	8.2	0.0	11.3	8.0	7.8	5.9	0.0	1.5	14.9	14.8
Brain (Amygdala) Pool	3.7	0.8	7.7	6.2	4.8	6.0	7.9	4.4	1.1	5.3
Brain (cerebellum)	12.0	0.4	19.8	10.7	9.7	11.5	1.8	1.2	1.4	9.7
Brain (fetal)	4.2	0.7	12.7	6.6	5.6	6.2	8.4	2.1	1.1	6.4
Brain (Hippocampus) Pool	7.5	3.2	11.7	8.6	6.9	8.3	9.9	4.3	2.0	10.2
Cerebral Cortex Pool	9.7	0.6	11.0	7.5	0.7	7.0	1.8	2.0	2.0	8.7
Brain (Substantia nigra) Pool	7.4	2.2	11.7	10.4	4.7	10.1	4.2	2.0	1.1	9.3
Brain (Thalamus) Pool	7.6	2.7	13.2	9.3	0.2	8.5	9.1	2.8	3.2	8.7
Brain (whole)	6.1	0.4	10.6	5.8	0.3	4.9	3.3	1.9	1.9	8.7
Spinal Cord Pool	10.1	2.3	14.7	11.0	7.6	12.1	13.1	4.2	2.9	9.0
Adrenal Gland	3.5	0.3	9.9	3.9	3.7	6.4	7.4	0.9	0.7	4.1
Pituitary gland Pool	0.9	0.0	1.1	1.2	1.1	0.8	1.8	0.6	0.4	0.5

Salivary Gland	0.9	0.0	1.8	1.3	0.9	1.3	2.3	0.0	0.2	1.0
Thyroid (female)	2.0	0.3	3.1	2.5	2.5	3.5	3.3	1.3	0.8	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.8	0.7	0.6	1.0	0.5	0.6	4.6	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.6	1.7	3.5	1.0	2.6	2.3

Table ARQ. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6433, Run 268713319	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6446, Run 268761804	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.6	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.6	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.5	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.0	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	0.0	0.0	0.4	0.0
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0

CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	0.3	0.8	3.7	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	0.8	1.6	0.0	0.0
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0	0.0	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells rest	5.6	5.0	2.7	11.8	3.8	6.4	6.1	19.5	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0	1.1	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	6.3	4.3	6.1	41.5	0.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	0.0	0.0	0.0	0.0

Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	0.7	0.9	2.1	0.0
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.9	0.0	5.8	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	2.6	2.9	5.8	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.3	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.6	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	10.2	0.0	3.6	0.0
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.6	1.0	0.0	0.0
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	4.2	0.7	**100.0**	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	1.6	0.0	2.4	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	0.3	1.6	4.3	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	1.0	0.0	1.6	0.4

Macrophages rest	0.9	1.8	0.0	0.6	0.6	1.4	0.0	6.9	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	2.1	0.8	6.5	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	1.5	0.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	1.0	54.3
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	74.2	97.3	74.7	65.1	97.9	1.4	**100.0**
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	2.2	5.1	15.3	0.6
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0	0.0	1.4	0.0

NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	1.1	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	28.5	62.9	3.1	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	19.3	25.2	0.4	28.3
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	25.9	23.3	0.9	16.0
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	25.9	20.4	2.0	9.3
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	16.0	15.0	1.3	4.3
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	25.0	29.9	1.0	25.2
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	2.3	5.6	1.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	5.1	0.8	0.0	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	1.4	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	13.6	20.0	0.0	4.9

Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	13.9	22.7	1.4	13.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	19.8	20.7	1.6	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	0.0	1.2	0.0	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0
Colon	7.9	4.7	4.0	4.6	9.5	7.0	7.9	1.8	4.8
Lung	2.2	1.2	0.0	2.8	4.6	1.3	1.6	0.8	0.0
Thymus	3.1	0.8	0.0	0.0	0.4	0.0	2.0	0.0	0.0
Kidney	4.2	4.4	4.9	7.8	9.7	5.3	10.2	50.0	0.6

Table ARR. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0

Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6431/Ag6435/Ag6440/Ag6442/Ag6446/ Ag6447 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal

muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

Summary: Ag6413/Ag6425/Ag6428/Ag6430/Ag6431/Ag6440/Ag6442/ Ag6446/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, ovarian cancer IGROV-1 cell line, lung cancer LX-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6433/Ag6439/Ag6442 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics

with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AS. CG56054-12: Integrin alpha 7-like protein.

Expression of gene CG56054-12 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6439, Ag6413 and Ag6964, described in Tables ASA, ASB, ASC, ASD, ASE, ASF, ASG, ASH, ASI and ASJ. Results of the RTQ-PCR runs are shown in Tables ASK, ASL, ASM, ASN, ASO and ASP.

Table ASA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2435	570
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2457	571
Reverse	5'-aacagcagctctacctccagtt-3'	22	2491	572

Table ASB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2874	573
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2913	574
Reverse	5'-gcgcagtccagggtg-3'	15	2999	575

Table ASC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	576
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	577
Reverse	5'-aaaagcaacccttccaa-3'	18	824	578

Table ASD. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3389	579
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3421	580
Reverse	5'-gccctggatgcccat-3'	15	3440	581

Table ASE. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	582

Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	583
Reverse	5'-agggagtagccgaagctct-3'	19	1471	584

Table ASF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	585
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	586
Reverse	5'-gggagccggtcagca-3'	15	899	587

Table ASG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2993	588
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	3034	589
Reverse	5'-ccgcgcggtcaaa-3'	13	3060	590

Table ASH. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	3250	591
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3270	592
Reverse	5'-gaagaatcccatcttccacag-3'	21	3336	593

Table ASI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	2073	594

Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2124	595
Reverse	5'-gctgttgttccatccacatc-3'	20	2166	596

Table ASJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	3079	597
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	3050	598
Reverse	5'-gccaactgtgtggtgttca-3'	19	3024	599

Table ASK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	21.6	19.2
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	28.9	49.7
AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	6.1	20.4
AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	17.6	5.6
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	42.6	57.4
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	32.5	28.5
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	37.9	86.5
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	6.4	0.0
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	24.5	16.8
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	27.5	21.6

AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	9.0	5.7
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	30.4	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	38.7	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	47.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	50.3	59.9
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	24.0	46.7
Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	14.9	50.0
Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	16.5	9.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	23.8	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	39.8	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	24.8	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	11.9	31.0

Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	21.6	39.5
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	16.0	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	10.2	4.9
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	18.6	11.1
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	22.7	42.3
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	22.1	14.8
Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	7.2	8.8
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	29.3	82.4
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	19.2	8.8
Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	13.6	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	39.5	**100.0**
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	7.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	5.9	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.4	32.8
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	15.7	9.2
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	37.1	28.1

Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	10.8	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	37.9	69.3
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	18.7	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	12.0	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	27.9	27.5

Table ASL. General_screening_panel_v1.4

Tissue Name	**Rel. Exp.(%) Ag4983, Run 218328386**	**Tissue Name**	**Rel. Exp.(%) Ag4983, Run 218328386**
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4

Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9

Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ASM. General_screening_panel_v1.5

Tissue Name	**Rel. Exp.(%) Ag6442, Run 264979530**	**Tissue Name**	**Rel. Exp.(%) Ag6442, Run 264979530**
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3

Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5

Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ASN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	2.6	20.0	8.2	17.4	13.8	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	0.0	2.0	0.5	0.8	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.0	0.2	4.1	0.6	2.5	2.2	2.9	2.4
Melanoma* M14	0.3	0.0	0.0	0.7	0.7	0.4	0.4	0.4	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	0.0	2.2	30.4	22.5	18.2	14.6	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.1
Testis Pool	5.2	0.0	3.5	8.8	4.2	10.4	9.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	0.5	2.5	1.0	1.9	1.8	1.3	4.3
Prostate Pool	8.1	0.0	1.0	11.5	8.5	11.3	12.1	28.5	10.0
Placenta	0.5	0.0	0.0	0.7	0.1	0.1	0.1	0.5	0.4
Uterus Pool	2.2	0.0	1.5	4.5	2.6	4.6	4.5	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	0.3	1.1	0.8	0.7	1.1	1.6	4.0
Ovarian ca. SK-OV-3	0.8	0.0	0.2	1.7	1.5	0.8	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.0	0.9	0.5	0.4	0.8	0.9	0.5
Ovarian ca. OVCAR-5	1.6	0.0	1.3	2.9	1.5	1.3	1.7	1.4	7.9

Ovarian ca. IGROV-1	**100.0**	**100.0**	**100.0**	77.9	90.8	84.7	97.9	69.3	75.8
Ovarian ca. OVCAR-8	13.6	5.6	21.9	14.0	11.9	15.6	14.6	17.3	16.7
Ovary	2.7	0.0	0.3	5.2	2.1	3.1	2.3	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.0	0.3	0.4	0.1	0.2	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.0	0.4	0.4	0.2	0.2	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.0	0.5	0.3	0.1	0.5	0.6	0.4
Breast ca. T47D	0.0	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.5
Breast ca. MDA-N	0.6	0.0	0.0	0.7	0.7	0.6	0.6	0.6	0.8
Breast Pool	15.0	0.0	4.1	21.8	19.5	14.6	10.7	12.2	16.7
Trachea	4.5	0.0	0.7	8.4	2.9	4.8	4.2	4.7	5.6
Lung	2.8	0.0	0.7	2.3	1.3	4.2	3.2	3.9	5.1
Fetal Lung	3.9	0.0	0.3	9.1	4.0	5.0	4.8	5.3	6.1
Lung ca. NCI-N417	2.0	2.0	0.9	3.5	2.7	3.3	2.6	4.0	2.3
Lung ca. LX-1	3.5	3.1	2.7	6.5	7.0	5.0	3.5	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.0	0.3	0.5	0.1	0.2	0.1	0.1
Lung ca. SHP-77	4.0	2.3	0.4	6.8	6.3	5.3	4.5	4.5	3.8
Lung ca. A549	0.3	0.0	2.6	0.9	0.3	0.0	0.4	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.0	0.9	0.7	0.6	0.3	0.4	0.5
Lung ca. NCI-H23	2.9	0.0	1.0	4.6	4.5	4.8	3.2	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.0	0.5	0.6	1.0	0.6	0.5	0.7

Lung ca. NCI-H522	1.7	0.0	0.6	2.3	2.4	1.7	1.3	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.0	0.3	1.1	0.6	0.6	0.5	0.8	8.2
Liver ca. HepG2	0.1	0.0	0.3	0.2	0.1	0.0	0.2	0.1	2.4
Kidney Pool	27.9	6.5	0.0	47.0	34.9	33.9	28.1	43.2	32.8
Fetal Kidney	1.4	0.0	0.0	4.9	5.1	4.1	4.0	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.0	0.2	0.2	0.3	0.1	0.3	0.9
Renal ca. A498	0.0	0.0	1.8	0.2	0.1	0.0	0.3	0.5	8.5
Renal ca. ACHN	1.5	0.0	0.5	2.5	0.7	1.7	1.5	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.0	0.5	0.3	0.2	0.2	0.6	0.3
Renal ca. TK-10	1.9	0.0	0.4	3.1	2.5	2.0	1.9	2.1	4.6
Bladder	4.2	0.0	0.0	5.9	3.0	5.5	5.1	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.0	1.7	1.7	0.9	1.2	1.1	6.7
Gastric ca. KATO III	0.4	0.0	0.5	0.8	0.4	0.2	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.0	1.5	0.2	0.0	0.2	0.2	0.3	1.2
Colon ca. SW480	20.9	9.5	5.2	41.8	39.0	27.0	23.3	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	4.8	16.4	15.5	12.8	10.3	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.3
Colon ca. HCT-116	2.1	1.6	0.2	3.2	3.8	2.5	2.0	2.1	4.3
Colon ca. CaCo-2	15.0	10.4	3.6	27.0	22.2	19.1	16.7	18.3	38.2
Colon cancer tissue	9.0	0.0	3.3	11.0	6.5	11.9	7.6	7.7	20.4

Colon ca. SW1116	1.3	0.0	3.0	2.5	1.7	2.0	1.5	1.8	6.0
Colon ca. Colo-205	0.1	0.0	0.4	0.3	0.2	0.2	0.0	0.2	0.8
Colon ca. SW-48	0.8	0.0	3.6	1.4	1.3	1.5	1.5	1.4	2.6
Colon Pool	20.3	0.0	5.0	28.1	28.7	23.2	18.7	25.5	20.6
Small Intestine Pool	14.0	0.0	1.7	17.1	10.5	11.2	13.0	12.8	10.4
Stomach Pool	8.1	0.0	2.3	14.3	6.2	9.5	9.3	8.5	10.7
Bone Marrow Pool	6.8	0.0	1.6	14.3	11.3	10.2	8.7	18.7	12.5
Fetal Heart	10.1	0.0	2.3	25.5	24.3	24.5	21.8	33.7	20.7
Heart Pool	28.7	5.2	7.0	29.7	23.0	25.9	17.2	33.7	26.1
Lymph Node Pool	17.6	0.0	6.1	33.7	30.4	22.1	23.7	19.9	24.7
Fetal Skeletal Muscle	31.9	36.9	5.2	54.3	46.7	48.6	46.3	19.1	50.7
Skeletal Muscle Pool	17.4	12.3	9.2	29.3	21.5	29.5	25.9	22.1	32.3
Spleen Pool	0.9	0.0	0.0	1.9	2.0	2.0	1.7	2.7	3.1
Thymus Pool	4.4	0.0	2.0	10.4	7.5	8.1	9.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	1.5	14.9	6.1	10.7	10.0	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	0.3	4.7	2.9	3.8	3.1	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	0.0	2.6	1.7	2.1	1.0	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.0	0.2	0.1	0.2	0.1	0.1

CNS cancer (astro) SNB-75	8.1	1.9	1.1	14.9	5.9	6.5	10.0	11.7	9.7
CNS cancer (glio) SNB-19	79.6	84.1	79.0	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**
CNS cancer (glio) SF-295	8.2	1.8	0.0	11.3	9.0	8.0	7.8	8.2	14.8
Brain (Amygdala) Pool	3.7	2.3	0.8	7.7	6.9	6.2	4.8	8.0	5.3
Brain (cerebellum)	12.0	6.6	0.4	19.8	11.1	10.7	9.7	8.8	9.7
Brain (fetal)	4.2	3.0	0.7	12.7	11.5	6.6	5.6	6.8	6.4
Brain (Hippocampus) Pool	7.5	3.1	3.2	11.7	11.0	8.6	6.9	11.0	10.2
Cerebral Cortex Pool	9.7	1.7	0.6	11.0	7.5	7.5	0.7	11.6	8.7
Brain (Substantia nigra) Pool	7.4	1.8	2.2	11.7	8.5	10.4	4.7	10.0	9.3
Brain (Thalamus) Pool	7.6	0.0	2.7	13.2	10.0	9.3	0.2	9.7	8.7
Brain (whole)	6.1	0.0	0.4	10.6	8.0	5.8	0.3	5.6	8.7
Spinal Cord Pool	10.1	3.2	2.3	14.7	12.8	11.0	7.6	12.2	9.0
Adrenal Gland	3.5	0.0	0.3	9.9	6.1	3.9	3.7	4.8	4.1
Pituitary gland Pool	0.9	0.0	0.0	1.1	0.8	1.2	1.1	1.4	0.5
Salivary Gland	0.9	0.0	0.0	1.8	1.1	1.3	0.9	1.1	1.0
Thyroid (female)	2.0	0.0	0.3	3.1	0.8	2.5	2.5	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.0	0.8	0.8	0.7	0.6	0.7	2.2

Pancreas Pool	1.2	0.0	0.0	2.0	1.1	1.1	1.6	3.2	2.3

Table ASO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	1.2
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2
LAK cells rest	5.6	5.0	2.7	11.8	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0

LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	1.4
Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	2.6
Macrophages rest	0.9	1.8	0.0	0.6	0.6	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	9.2

LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	1.4
Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	2.6
Macrophages rest	0.9	1.8	0.0	0.6	0.6	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	9.2

HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	1.5	0.0
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	74.2	97.3	74.7	95.9

KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	8.5
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	96.6
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	26.6

Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	47.3
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.0	4.6	9.5	8.4
Lung	2.2	1.2	0.0	2.8	4.6	2.1
Thymus	3.1	0.8	0.0	0.0	0.4	2.4
Kidney	4.2	4.4	4.9	7.8	9.7	5.2

Table ASP. general oncology screening panel_v_2.4

Tissue Name	**Rel. Exp.(%) Ag4983, Run 260281959**	**Rel. Exp.(%) Ag6442, Run 264979180**	**Tissue Name**	**Rel. Exp.(%) Ag4983, Run 260281959**	**Rel. Exp.(%) Ag6442, Run 264979180**
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9

Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6424/Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/Ag6424/ Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. Highest

expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AT. CG56054-13: Integrin alpha 7-like protein.

Expression of gene CG56054-13 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6440, Ag6446, Ag6413 and

Ag6964, described in Tables ATA, ATB, ATC, ATD, ATE, ATF, ATG, ATH, ATI, ATJ and ATK. Results of the RTQ-PCR runs are shown in Tables ATL, ATM, ATN, ATO, ATP and ATQ.

Table ATA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2330	600
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2352	601
Reverse	5'-aacagcagctctacctccagtt-3'	22	2386	602

Table ATB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2769	603
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2808	604
Reverse	5'-gcgcagtccagggtg-3'	15	2894	605

Table ATC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	637	606
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	656	607
Reverse	5'-aaaagcaacccccttccaa-3'	18	719	608

Table ATD. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3504	609
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3536	610

Reverse	5'-gccctggatgcccat-3'	15	3555	611

Table ATE. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1289	612
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1329	613
Reverse	5'-agggagtagccgaagctct-3'	19	1366	614

Table ATF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	738	615
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	761	616
Reverse	5'-gggagccggtcagca-3'	15	794	617

Table ATG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2888	618
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2929	619
Reverse	5'-ccgcgcggtcaaa-3'	13	2955	620

Table ATH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	3461	621
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	3528	622
Reverse	5'-ccctggatgcccatc-3'	15	3554	623

Table ATI. Probe Name Ag6446

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcttcttccatcggagca-3'	18	3244	624
Probe	TET-5'-caactatcaccgggcctgtctggc-3'-TAMRA	24	3284	625
Reverse	5'-catggctgaaggctgca-3'	17	3310	626

Table ATJ. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1968	627
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2019	628
Reverse	5'-gctgttgttccatccacatc-3'	20	2061	629

Table ATK. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2974	630
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2945	631
Reverse	5'-gccaactgtgtggtgttca-3'	19	2919	632

Table ATL. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6446, Run 269254006
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	18.9	19.2	42.9
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	61.1	49.7	41.8

AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	9.7	20.4	23.7
AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	23.3	5.6	29.9
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	34.6	57.4	67.8
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1	**100.0**
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	29.9	28.5	39.2
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	54.7	86.5	62.4
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	5.8	0.0	14.6
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	12.6	16.8	72.7
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	59.0	21.6	43.2
AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	17.1	5.7	36.3
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	29.9	8.7	43.2
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7	63.3
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	39.2	55.9	95.3
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	48.6	76.8	45.1
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	17.0	59.9	30.6
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	23.3	46.7	5.9

Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	43.5	50.0	13.6
Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	9.2	9.5	12.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	30.1	13.6	26.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	51.1	46.0	21.2
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	7.2	0.0	27.2
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	9.9	31.0	24.5
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	14.9	39.5	19.2
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	5.8	6.3	39.5
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	7.8	4.9	19.3
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	35.4	11.1	25.3
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	16.6	42.3	25.2
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	23.5	14.8	9.7

Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	15.2	8.8	6.5
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	35.8	82.4	8.1
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	4.4	8.8	15.8
Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	12.9	24.0	23.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	22.4	**100.0**	23.3
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	5.0	9.3	15.6
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	6.7	4.1	4.5
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.9	32.8	5.9
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	33.2	9.2	5.7
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	17.4	28.1	74.2
Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	21.6	9.1	8.6
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	47.3	69.3	24.0
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	17.1	37.6	23.7
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	11.7	10.4	11.0

Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	29.3	27.5	27.0

Table ATM. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3

Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ATN. General_screening_panel_v1.5

Tissue Name	**Rel. Exp.(%) Ag6442, Run 264979530**	**Tissue Name**	**Rel. Exp.(%) Ag6442, Run 264979530**

Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2

Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ATO. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6446, Run 277250179	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	2.6	20.0	8.2	17.4	13.8	3.7	1.7	18.8
Melanoma* Hs688(A).T	0.5	0.0	0.0	2.0	0.5	0.8	0.9	0.0	0.1	0.7

Melanoma* Hs688(B).T	2.7	0.0	0.2	4.1	0.6	2.5	2.2	0.8	0.1	2.4
Melanoma* M14	0.3	0.0	0.0	0.7	0.7	0.4	0.4	0.0	0.1	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.1
Melanoma* SK-MEL-5	15.2	0.0	2.2	30.4	22.5	18.2	14.6	3.0	6.8	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	0.0	3.5	8.8	4.2	10.4	9.0	3.0	5.8	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	0.5	2.5	1.0	1.9	1.8	1.2	7.7	4.3
Prostate Pool	8.1	0.0	1.0	11.5	8.5	11.3	12.1	2.1	1.9	10.0
Placenta	0.5	0.0	0.0	0.7	0.1	0.1	0.1	0.0	0.9	0.4
Uterus Pool	2.2	0.0	1.5	4.5	2.6	4.6	4.5	2.3	0.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	0.3	1.1	0.8	0.7	1.1	0.4	4.8	4.0
Ovarian ca. SK-OV-3	0.8	0.0	0.2	1.7	1.5	0.8	0.9	0.5	2.5	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.0	0.9	0.5	0.4	0.8	0.0	0.5	0.5
Ovarian ca. OVCAR-5	1.6	0.0	1.3	2.9	1.5	1.3	1.7	4.2	15.6	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	**100.0**	77.9	90.8	84.7	97.9	**100.0**	5.4	75.8
Ovarian ca. OVCAR-8	13.6	5.6	21.9	14.0	11.9	15.6	14.6	18.2	4.2	16.7
Ovary	2.7	0.0	0.3	5.2	2.1	3.1	2.3	0.8	0.2	2.4
Breast ca. MCF-7	0.3	0.0	0.0	0.3	0.4	0.1	0.2	0.3	0.9	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.0	0.4	0.4	0.2	0.2	0.0	0.2	0.3

Breast ca. BT 549	0.5	0.0	0.0	0.5	0.3	0.1	0.5	0.0	0.2	0.4
Breast ca. T47D	0.0	0.0	0.0	0.5	0.3	0.2	0.3	0.3	0.7	0.5
Breast ca. MDA-N	0.6	0.0	0.0	0.7	0.7	0.6	0.6	0.3	0.0	0.8
Breast Pool	15.0	0.0	4.1	21.8	19.5	14.6	10.7	3.5	2.0	16.7
Trachea	4.5	0.0	0.7	8.4	2.9	4.8	4.2	1.4	0.5	5.6
Lung	2.8	0.0	0.7	2.3	1.3	4.2	3.2	5.3	0.5	5.1
Fetal Lung	3.9	0.0	0.3	9.1	4.0	5.0	4.8	2.9	0.5	6.1
Lung ca. NCI-N417	2.0	2.0	0.9	3.5	2.7	3.3	2.6	2.0	0.4	2.3
Lung ca. LX-1	3.5	3.1	2.7	6.5	7.0	5.0	3.5	6.3	**100.0**	44.1
Lung ca. NCI-H146	0.1	0.0	0.0	0.3	0.5	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	2.3	0.4	6.8	6.3	5.3	4.5	0.8	0.1	3.8
Lung ca. A549	0.3	0.0	2.6	0.9	0.3	0.0	0.4	2.2	14.3	4.7
Lung ca. NCI-H526	0.2	0.0	0.0	0.9	0.7	0.6	0.3	0.3	0.0	0.5
Lung ca. NCI-H23	2.9	0.0	1.0	4.6	4.5	4.8	3.2	2.3	15.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.1	0.3
Lung ca. HOP-62	0.5	0.0	0.0	0.5	0.6	1.0	0.6	0.0	0.2	0.7
Lung ca. NCI-H522	1.7	0.0	0.6	2.3	2.4	1.7	1.3	2.5	27.7	8.9
Liver	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.4	5.3	2.0
Fetal Liver	0.3	0.0	0.3	1.1	0.6	0.6	0.5	0.8	23.0	8.2
Liver ca. HepG2	0.1	0.0	0.3	0.2	0.1	0.0	0.2	0.9	7.3	2.4
Kidney Pool	27.9	6.5	0.0	47.0	34.9	33.9	28.1	14.6	5.3	32.8
Fetal Kidney	1.4	0.0	0.0	4.9	5.1	4.1	4.0	3.4	20.2	11.5

Renal ca. 786-0	0.2	0.0	0.0	0.2	0.2	0.3	0.1	0.0	1.7	0.9
Renal ca. A498	0.0	0.0	1.8	0.2	0.1	0.0	0.3	3.8	23.0	8.5
Renal ca. ACHN	1.5	0.0	0.5	2.5	0.7	1.7	1.5	0.5	3.8	2.5
Renal ca. UO-31	0.3	0.0	0.0	0.5	0.3	0.2	0.2	0.0	0.7	0.3
Renal ca. TK-10	1.9	0.0	0.4	3.1	2.5	2.0	1.9	0.5	6.4	4.6
Bladder	4.2	0.0	0.0	5.9	3.0	5.5	5.1	0.9	3.2	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.0	1.7	1.7	0.9	1.2	0.8	17.8	6.7
Gastric ca. KATO III	0.4	0.0	0.5	0.8	0.4	0.2	0.3	0.4	1.3	0.9
Colon ca. SW-948	0.0	0.0	1.5	0.2	0.0	0.2	0.2	2.2	6.1	1.2
Colon ca. SW480	20.9	9.5	5.2	41.8	39.0	27.0	23.3	6.3	39.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	4.8	16.4	15.5	12.8	10.3	7.2	71.2	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.0	0.2	0.2	0.3	3.5	0.3
Colon ca. HCT-116	2.1	1.6	0.2	3.2	3.8	2.5	2.0	0.6	6.4	4.3
Colon ca. CaCo-2	15.0	10.4	3.6	27.0	22.2	19.1	16.7	6.5	78.5	38.2
Colon cancer tissue	9.0	0.0	3.3	11.0	6.5	11.9	7.6	4.4	21.9	20.4
Colon ca. SW1116	1.3	0.0	3.0	2.5	1.7	2.0	1.5	2.1	19.5	6.0
Colon ca. Colo-205	0.1	0.0	0.4	0.3	0.2	0.2	0.0	1.3	3.0	0.8
Colon ca. SW-48	0.8	0.0	3.6	1.4	1.3	1.5	1.5	3.0	4.2	2.6
Colon Pool	20.3	0.0	5.0	28.1	28.7	23.2	18.7	8.1	3.1	20.6

Small Intestine Pool	14.0	0.0	1.7	17.1	10.5	11.2	13.0	2.0	2.5	10.4
Stomach Pool	8.1	0.0	2.3	14.3	6.2	9.5	9.3	4.2	1.1	10.7
Bone Marrow Pool	6.8	0.0	1.6	14.3	11.3	10.2	8.7	3.5	1.1	12.5
Fetal Heart	10.1	0.0	2.3	25.5	24.3	24.5	21.8	8.6	2.7	20.7
Heart Pool	28.7	5.2	7.0	29.7	23.0	25.9	17.2	10.7	3.4	26.1
Lymph Node Pool	17.6	0.0	6.1	33.7	30.4	22.1	23.7	6.7	2.8	24.7
Fetal Skeletal Muscle	31.9	36.9	5.2	54.3	46.7	48.6	46.3	19.2	57.0	50.7
Skeletal Muscle Pool	17.4	12.3	9.2	29.3	21.5	29.5	25.9	22.7	24.3	32.3
Spleen Pool	0.9	0.0	0.0	1.9	2.0	2.0	1.7	0.6	2.6	3.1
Thymus Pool	4.4	0.0	2.0	10.4	7.5	8.1	9.4	3.1	1.4	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	1.5	14.9	6.1	10.7	10.0	2.2	6.3	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	0.3	4.7	2.9	3.8	3.1	0.8	5.1	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	0.0	2.6	1.7	2.1	1.0	0.5	3.9	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.0	0.2	0.1	0.2	0.2	0.3	0.1
CNS cancer (astro) SNB-75	8.1	1.9	1.1	14.9	5.9	6.5	10.0	2.8	2.4	9.7
CNS cancer (glio) SNB-19	79.6	84.1	79.0	**100.0**	**100.0**	**100.0**	**100.0**	97.9	5.2	**100.0**

CNS cancer (glio) SF-295	8.2	1.8	0.0	11.3	9.0	8.0	7.8	1.5	14.9	14.8
Brain (Amygdala) Pool	3.7	2.3	0.8	7.7	6.9	6.2	4.8	4.4	1.1	5.3
Brain (cerebellum)	12.0	6.6	0.4	19.8	11.1	10.7	9.7	1.2	1.4	9.7
Brain (fetal)	4.2	3.0	0.7	12.7	11.5	6.6	5.6	2.1	1.1	6.4
Brain (Hippocampus) Pool	7.5	3.1	3.2	11.7	11.0	8.6	6.9	4.3	2.0	10.2
Cerebral Cortex Pool	9.7	1.7	0.6	11.0	7.5	7.5	0.7	2.0	2.0	8.7
Brain (Substantia nigra) Pool	7.4	1.8	2.2	11.7	8.5	10.4	4.7	2.0	1.1	9.3
Brain (Thalamus) Pool	7.6	0.0	2.7	13.2	10.0	9.3	0.2	2.8	3.2	8.7
Brain (whole)	6.1	0.0	0.4	10.6	8.0	5.8	0.3	1.9	1.9	8.7
Spinal Cord Pool	10.1	3.2	2.3	14.7	12.8	11.0	7.6	4.2	2.9	9.0
Adrenal Gland	3.5	0.0	0.3	9.9	6.1	3.9	3.7	0.9	0.7	4.1
Pituitary gland Pool	0.9	0.0	0.0	1.1	0.8	1.2	1.1	0.6	0.4	0.5
Salivary Gland	0.9	0.0	0.0	1.8	1.1	1.3	0.9	0.0	0.2	1.0
Thyroid (female)	2.0	0.0	0.3	3.1	0.8	2.5	2.5	1.3	0.8	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.0	0.8	0.8	0.7	0.6	0.6	4.6	2.2
Pancreas Pool	1.2	0.0	0.0	2.0	1.1	1.1	1.6	1.0	2.6	2.3

Table ATP. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577
Secondary Th1 act	0.1	0.3	0.0	1.3	0.0	0.7
Secondary Th2 act	0.5	0.3	0.0	1.2	0.0	0.8
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.0	0.7
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.0	0.4
Primary Tr1 act	0.1	0.0	0.0	0.7	0.0	0.7
Primary Th1 rest	0.0	0.0	0.0	0.1	0.0	0.3
Primary Th2 rest	0.0	0.0	0.0	0.4	0.0	0.2
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	0.0	2.4
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.0	0.7
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.0	0.3
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.0	0.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0
LAK cells rest	5.6	5.0	2.7	11.8	0.1	3.8
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	0.1	6.3
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	0.0	2.5
Two Way MLR 3 day	1.4	1.1	0.0	2.2	0.0	1.3
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.0	0.9
Two Way MLR 7 day	2.3	0.7	13.2	1.1	0.0	2.6
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.0	0.7
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.0	0.2
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	0.1	8.1
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	0.0	2.7
Dendritic cells none	5.6	3.1	13.8	4.1	0.0	5.3
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.0	0.7
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.0	0.2
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	0.0	1.8
Macrophages rest	0.9	1.8	0.0	0.6	0.0	0.6
Macrophages LPS	7.5	4.0	0.0	5.4	0.1	6.3
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.0	0.3

HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.0	0.5
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.0	0.4
HUVEC IL-11	0.0	0.0	0.0	0.4	0.0	0.3
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	0.0	1.5
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	12.0	**100.0**
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	74.2	97.3	**100.0**	74.7
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.0	0.4
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.0	0.8
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	0.0	6.7
NCI-H292 none	0.3	0.3	0.0	1.7	0.0	0.6
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.0	0.5
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.0	0.5
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.0	0.9
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.0	0.6
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	0.2	65.5
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	0.1	39.8
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	0.1	21.2
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	0.1	26.8
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	0.0	10.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	0.2	46.3
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	0.0	6.3
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.0	0.8
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	0.0	1.3
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	0.1	20.2
Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	0.1	19.8
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	0.1	46.7

Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.0	0.4
Neutrophils rest	0.1	0.0	0.0	0.0	0.0	0.3
Colon	7.9	4.7	4.0	4.6	0.0	9.5
Lung	2.2	1.2	0.0	2.8	0.0	4.6
Thymus	3.1	0.8	0.0	0.0	0.0	0.4
Kidney	4.2	4.4	4.9	7.8	0.1	9.7

Table ATQ. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2

Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/ Ag6428/Ag6430/Ag6431/Ag6440/Ag6442/Ag6446 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6424/ Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/ Ag6424/Ag6425/ Ag6428/Ag6431/Ag6440/ Ag6446/Ag6964 Highest expression of this gene is detected in skeletal muscle, ovarian cancer IGROV-1 cell line, lung cancer LX-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary: Ag4983/Ag6413/Ag6425/Ag6428/Ag6431 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types

and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424/Ag6440 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AU. CG56054-14: Integrin alpha 7-like protein.

Expression of gene CG56054-14 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6428, Ag6429, Ag6431, Ag6435, Ag6439, Ag6447, Ag6413 and Ag6964, described in Tables AUA, AUB, AUC, AUD, AUE, AUF, AUG, AUH, AUI and AUJ. Results of the RTQ-PCR runs are shown in Tables AUK, AUL, AUM, AUN, AUO and AUP.

Table AUA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	633

Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	634
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	635

Table AUB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	636
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	637
Reverse	5'-gcgcagtccagggtg-3'	15	2906	638

Table AUC. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	639
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	640
Reverse	5'-agggagtagccgaagctct-3'	19	1378	641

Table AUD. Probe Name Ag6429

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgtgccccagtaccat-3'	17	3289	642
Probe	TET-5'-cgggcaccatcctgaggaacaac-3'-TAMRA	23	3355	643
Reverse	5'-gggcccagccaggat-3'	15	3391	644

Table AUE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	645
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	646

Reverse	5'-ccgcgcggtcaaa-3'	13	2967	647

Table AUF. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	648
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	649
Reverse	5'-cagggaccgggatga-3'	15	829	650

Table AUG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	3157	651
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3177	652
Reverse	5'-gaagaatcccatcttccacag-3'	21	3243	653

Table AUH. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	654
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	655
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	656

Table AUI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	657
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	658
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	659

Table AUJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	660
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	661
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	662

Table AUK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	18.0	18.8	17.1	21.6	19.2	18.8
AD 2 Hippo	41.2	52.9	32.3	28.7	27.9	28.9	49.7	10.4
AD 3 Hippo	8.9	6.4	3.7	7.5	4.8	6.1	20.4	0.0
AD 4 Hippo	14.8	25.5	10.7	18.8	18.3	17.6	5.6	4.6
AD 5 Hippo	44.8	41.8	53.2	38.4	46.7	42.6	57.4	11.0
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1	**100.0**
Control 2 Hippo	24.3	36.1	18.7	29.5	8.5	32.5	28.5	3.1
Control 4 Hippo	42.9	43.8	27.0	32.3	29.9	37.9	86.5	43.8
Control (Path) 3 Hippo	14.2	11.4	4.6	6.0	5.2	6.4	0.0	5.3
AD 1 Temporal Ctx	23.3	15.9	12.9	17.1	12.8	24.5	16.8	9.0
AD 2 Temporal Ctx	41.5	47.3	31.0	39.8	45.1	27.5	21.6	21.0

AD 3 Temporal Ctx	9.5	9.8	6.0	11.3	4.1	9.0	5.7	3.9
AD 4 Temporal Ctx	30.6	39.0	20.2	25.3	6.8	30.4	8.7	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	36.3	1.6	41.8	73.7	23.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	32.3	33.2	38.7	55.9	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	46.7	52.1	47.6	76.8	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	50.3	37.6	50.3	59.9	61.1
Control 1 Temporal Ctx	12.2	23.0	12.9	15.6	6.7	24.0	46.7	2.8
Control 2 Temporal Ctx	14.2	32.5	18.2	17.4	7.3	14.9	50.0	16.0
Control 3 Temporal Ctx	15.1	15.3	9.6	14.5	4.4	16.5	9.5	3.1
Control 3 Temporal Ctx	23.7	25.0	15.2	13.1	11.7	23.8	13.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	30.6	24.8	39.8	46.0	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	20.4	9.8	24.8	0.0	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	10.9	3.5	11.9	31.0	6.3

Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	18.2	14.8	21.6	39.5	7.0
AD 1 Occipital Ctx	16.0	11.9	10.2	11.5	15.0	16.0	6.3	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	8.8	8.0	10.2	4.9	0.0
AD 4 Occipital Ctx	18.9	23.7	13.0	17.9	6.8	18.6	11.1	3.5
AD 5 Occipital Ctx	24.8	28.3	25.3	22.5	12.7	22.7	42.3	3.8
AD 6 Occipital Ctx	20.6	31.9	20.2	17.0	5.9	22.1	14.8	8.5
Control 1 Occipital Ctx	9.5	14.4	6.0	8.7	4.1	7.2	8.8	1.3
Control 2 Occipital Ctx	31.9	42.6	26.4	33.2	20.3	29.3	82.4	13.7
Control 3 Occipital Ctx	18.8	13.0	10.7	17.1	7.5	19.2	8.8	5.0
Control 4 Occipital Ctx	18.2	17.0	12.0	12.6	3.3	13.6	24.0	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	36.1	25.9	39.5	**100.0**	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	7.9	7.4	7.0	9.3	13.2

Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	6.0	2.3	5.9	4.1	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	10.2	21.0	11.4	32.8	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	16.3	12.5	15.7	9.2	5.0
Control 2 Parietal Ctx	32.8	28.9	34.4	28.3	41.2	37.1	28.1	25.5
Control 3 Parietal Ctx	20.6	19.8	11.5	8.7	13.2	10.8	9.1	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	39.2	22.5	37.9	69.3	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	22.5	26.8	18.7	37.6	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	7.1	7.5	12.0	10.4	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	8.8	20.6	27.9	27.5	9.4

Table AUL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1

Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5

Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AUM. General_screening_panel_v1.5

Tissue Name	**Rel. Exp.(%) Ag6442, Run 264979530**	**Tissue Name**	**Rel. Exp.(%) Ag6442, Run 264979530**
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2

Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6

Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AUN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	20.0	17.4	13.8	13.2	17.3	18.8
Melanoma* Hs688(A).T	0.5	2.0	0.8	0.9	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	4.1	2.5	2.2	1.9	2.9	2.4
Melanoma* M14	0.3	0.7	0.4	0.4	0.0	0.4	0.7
Melanoma* LOXIMVI	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	30.4	18.2	14.6	4.4	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.1	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	8.8	10.4	9.0	10.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	2.5	1.9	1.8	1.8	1.3	4.3
Prostate Pool	8.1	11.5	11.3	12.1	10.0	28.5	10.0

Placenta	0.5	0.7	0.1	0.1	0.3	0.5	0.4
Uterus Pool	2.2	4.5	4.6	4.5	16.2	5.3	4.1
Ovarian ca. OVCAR-3	0.9	1.1	0.7	1.1	0.4	1.6	4.0
Ovarian ca. SK-OV-3	0.8	1.7	0.8	0.9	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.9	0.4	0.8	0.0	0.9	0.5
Ovarian ca. OVCAR-5	1.6	2.9	1.3	1.7	0.3	1.4	7.9
Ovarian ca. IGROV-1	**100.0**	77.9	84.7	97.9	27.0	69.3	75.8
Ovarian ca. OVCAR-8	13.6	14.0	15.6	14.6	7.6	17.3	16.7
Ovary	2.7	5.2	3.1	2.3	4.5	2.8	2.4
Breast ca. MCF-7	0.3	0.3	0.1	0.2	0.0	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.4	0.2	0.2	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.5	0.1	0.5	0.0	0.6	0.4
Breast ca. T47D	0.0	0.5	0.2	0.3	0.0	0.4	0.5
Breast ca. MDA-N	0.6	0.7	0.6	0.6	0.7	0.6	0.8
Breast Pool	15.0	21.8	14.6	10.7	42.9	12.2	16.7
Trachea	4.5	8.4	4.8	4.2	8.3	4.7	5.6
Lung	2.8	2.3	4.2	3.2	3.9	3.9	5.1
Fetal Lung	3.9	9.1	5.0	4.8	8.0	5.3	6.1
Lung ca. NCI-N417	2.0	3.5	3.3	2.6	0.2	4.0	2.3
Lung ca. LX-1	3.5	6.5	5.0	3.5	0.9	4.9	44.1
Lung ca. NCI-H146	0.1	0.3	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	6.8	5.3	4.5	0.2	4.5	3.8
Lung ca. A549	0.3	0.9	0.0	0.4	0.0	0.6	4.7

Lung ca. NCI-H526	0.2	0.9	0.6	0.3	0.0	0.4	0.5
Lung ca. NCI-H23	2.9	4.6	4.8	3.2	0.6	2.9	10.3
Lung ca. NCI-H460	0.0	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.5	1.0	0.6	0.0	0.5	0.7
Lung ca. NCI-H522	1.7	2.3	1.7	1.3	0.0	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	2.0
Fetal Liver	0.3	1.1	0.6	0.5	0.3	0.8	8.2
Liver ca. HepG2	0.1	0.2	0.0	0.2	0.0	0.1	2.4
Kidney Pool	27.9	47.0	33.9	28.1	**100.0**	43.2	32.8
Fetal Kidney	1.4	4.9	4.1	4.0	12.1	5.8	11.5
Renal ca. 786-0	0.2	0.2	0.3	0.1	0.0	0.3	0.9
Renal ca. A498	0.0	0.2	0.0	0.3	0.0	0.5	8.5
Renal ca. ACHN	1.5	2.5	1.7	1.5	0.0	1.2	2.5
Renal ca. UO-31	0.3	0.5	0.2	0.2	0.0	0.6	0.3
Renal ca. TK-10	1.9	3.1	2.0	1.9	0.7	2.1	4.6
Bladder	4.2	5.9	5.5	5.1	6.6	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	1.7	0.9	1.2	0.0	1.1	6.7
Gastric ca. KATO III	0.4	0.8	0.2	0.3	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.2	0.2	0.2	0.0	0.3	1.2
Colon ca. SW480	20.9	41.8	27.0	23.3	4.4	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	16.4	12.8	10.3	1.7	6.1	25.0
Colon ca. HT29	0.2	0.0	0.2	0.2	0.0	0.0	0.3
Colon ca. HCT-116	2.1	3.2	2.5	2.0	0.5	2.1	4.3

Colon ca. CaCo-2	15.0	27.0	19.1	16.7	7.6	18.3	38.2
Colon cancer tissue	9.0	11.0	11.9	7.6	5.6	7.7	20.4
Colon ca. SW1116	1.3	2.5	2.0	1.5	1.1	1.8	6.0
Colon ca. Colo-205	0.1	0.3	0.2	0.0	0.0	0.2	0.8
Colon ca. SW-48	0.8	1.4	1.5	1.5	0.0	1.4	2.6
Colon Pool	20.3	28.1	23.2	18.7	44.8	25.5	20.6
Small Intestine Pool	14.0	17.1	11.2	13.0	26.8	12.8	10.4
Stomach Pool	8.1	14.3	9.5	9.3	24.0	8.5	10.7
Bone Marrow Pool	6.8	14.3	10.2	8.7	25.9	18.7	12.5
Fetal Heart	10.1	25.5	24.5	21.8	31.6	33.7	20.7
Heart Pool	28.7	29.7	25.9	17.2	23.5	33.7	26.1
Lymph Node Pool	17.6	33.7	22.1	23.7	64.6	19.9	24.7
Fetal Skeletal Muscle	31.9	54.3	48.6	46.3	46.7	19.1	50.7
Skeletal Muscle Pool	17.4	29.3	29.5	25.9	24.7	22.1	32.3
Spleen Pool	0.9	1.9	2.0	1.7	2.4	2.7	3.1
Thymus Pool	4.4	10.4	8.1	9.4	18.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	14.9	10.7	10.0	5.8	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	4.7	3.8	3.1	1.5	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	2.6	2.1	1.0	0.7	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.1	0.2	0.2	0.1	0.1
CNS cancer (astro) SNB-75	8.1	14.9	6.5	10.0	3.1	11.7	9.7

CNS cancer (glio) SNB-19	79.6	100.0	100.0	100.0	12.8	100.0	100.0
CNS cancer (glio) SF-295	8.2	11.3	8.0	7.8	0.0	8.2	14.8
Brain (Amygdala) Pool	3.7	7.7	6.2	4.8	7.9	8.0	5.3
Brain (cerebellum)	12.0	19.8	10.7	9.7	1.8	8.8	9.7
Brain (fetal)	4.2	12.7	6.6	5.6	8.4	6.8	6.4
Brain (Hippocampus) Pool	7.5	11.7	8.6	6.9	9.9	11.0	10.2
Cerebral Cortex Pool	9.7	11.0	7.5	0.7	1.8	11.6	8.7
Brain (Substantia nigra) Pool	7.4	11.7	10.4	4.7	4.2	10.0	9.3
Brain (Thalamus) Pool	7.6	13.2	9.3	0.2	9.1	9.7	8.7
Brain (whole)	6.1	10.6	5.8	0.3	3.3	5.6	8.7
Spinal Cord Pool	10.1	14.7	11.0	7.6	13.1	12.2	9.0
Adrenal Gland	3.5	9.9	3.9	3.7	7.4	4.8	4.1
Pituitary gland Pool	0.9	1.1	1.2	1.1	1.8	1.4	0.5
Salivary Gland	0.9	1.8	1.3	0.9	2.3	1.1	1.0
Thyroid (female)	2.0	3.1	2.5	2.5	3.3	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.8	0.7	0.6	0.5	0.7	2.2
Pancreas Pool	1.2	2.0	1.1	1.6	3.5	3.2	2.3

Table AUO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806

Secondary Th1 act	0.1	0.3	1.3	0.7	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	1.2	0.8	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.3	0.4	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.7	0.7	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.1	0.3	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.4	0.2	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	5.4	2.4	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	1.5	0.7	1.6	2.3	0.0
CD8 lymphocyte act	0.4	0.9	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.4	0.3	0.0	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.5	0.4	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti -CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2	0.0
LAK cells rest	5.6	5.0	11.8	3.8	6.1	15.2	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.1	6.3	6.1	9.0	0.0
NK Cells IL-2 rest	0.9	0.1	3.4	2.5	0.0	1.4	0.0
Two Way MLR 3 day	1.4	1.1	2.2	1.3	0.9	1.4	0.0
Two Way MLR 5 day	4.5	0.9	0.8	0.9	0.0	0.0	0.0
Two Way MLR 7 day	2.3	0.7	1.1	2.6	2.9	3.7	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.6	0.7	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.7	0.2	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	29.1	8.1	0.0	68.8	0.0
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	2.7	1.0	1.8	0.0
Dendritic cells none	5.6	3.1	4.1	5.3	0.7	0.0	0.0
Dendritic cells LPS	1.6	0.3	1.0	0.7	0.0	0.0	0.0
Dendritic cells anti-CD40	2.0	1.6	0.5	0.2	1.6	0.0	0.0
Monocytes rest	0.2	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	5.7	1.8	0.0	2.6	0.4
Macrophages rest	0.9	1.8	0.6	0.6	0.0	0.0	0.0

Macrophages LPS	7.5	4.0	5.4	6.3	0.8	9.2	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.4	0.3	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	0.3	1.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	**100.0**	**100.0**	54.3

Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	97.3	74.7	97.9	95.9	**100.0**
KU-812 (Basophil) rest	0.1	0.0	0.0	0.4	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.8	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	2.6	6.7	5.1	8.5	0.6
NCI-H292 none	0.3	0.3	1.7	0.6	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.5	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.7	0.5	0.0	0.0	0.0
NCI-H292 IL-13	0.6	0.6	0.9	0.9	0.0	0.0	0.0
NCI-H292 IFN gamma	0.2	0.0	0.5	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	95.9	65.5	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	48.6	39.8	25.2	62.9	28.3
Lung fibroblast IL-4	26.1	28.7	27.4	21.2	23.3	34.9	16.0
Lung fibroblast IL-9	28.5	42.0	24.0	26.8	20.4	96.6	9.3
Lung fibroblast IL-13	31.6	14.6	11.9	10.4	15.0	13.4	4.3
Lung fibroblast IFN gamma	20.4	32.8	55.9	46.3	29.9	89.5	25.2

Dermal fibroblast CCD1070 rest	2.5	2.9	6.0	6.3	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	2.7	0.8	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	5.6	1.3	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	30.6	20.2	20.0	26.6	4.9
Dermal fibroblast IL-4	10.7	14.6	30.8	19.8	22.7	25.5	13.5
Dermal Fibroblasts rest	24.8	42.3	54.3	46.7	20.7	47.3	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.9	0.4	1.2	0.0	0.0
Neutrophils rest	0.1	0.0	0.0	0.3	0.0	0.0	0.0
Colon	7.9	4.7	4.6	9.5	7.9	8.4	4.8
Lung	2.2	1.2	2.8	4.6	1.6	2.1	0.0
Thymus	3.1	0.8	0.0	0.4	2.0	2.4	0.0
Kidney	4.2	4.4	7.8	9.7	10.2	5.2	0.6

Table AUP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9

Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/Ag6428/Ag6431/ Ag6435/Ag6439/Ag6442/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6429 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric,

colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/Ag6428/Ag6431/ Ag6435/Ag6439 Six experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-28.5). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen

in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6429/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D

Summary: Ag4983/Ag6413/Ag6428/Ag6431/Ag6435/Ag6439/Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this

gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AV. CG56054-15: Integrin alpha 7-like protein.

Expression of gene CG56054-15 was assessed using the primer-probe sets Ag6425, Ag6428, Ag6432, Ag6435 and Ag6447, described in Tables AVA, AVB, AVC, AVD and AVE. Results of the RTQ-PCR runs are shown in Tables AVF, AVG and AVH.

Table AVA. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1888	663
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1920	664
Reverse	5'-gccctggatgcccat-3'	15	1939	665

Table AVB. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	666
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	667
Reverse	5'-agggagtagccgaagctct-3'	19	1378	668

Table AVC. Probe Name Ag6432

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaccttgtcctacagtctccagac-3'	24	1841	669
Probe	TET-5'-tgcacaccccatcctggctgct-3'-TAMRA	22	1892	670
Reverse	5'-gctcgggatgcccgt-3'	15	1915	671

Table AVD. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	672

Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	673
Reverse	5'-cagggaccgggatga-3'	15	829	674

Table AVE. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	675
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	676
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	677

Table AVF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	18.0	17.1	18.8
AD 2 Hippo	32.3	27.9	10.4
AD 3 Hippo	3.7	4.8	0.0
AD 4 Hippo	10.7	18.3	4.6
AD 5 Hippo	53.2	46.7	11.0
AD 6 Hippo	**100.0**	**100.0**	**100.0**
Control 2 Hippo	18.7	8.5	3.1
Control 4 Hippo	27.0	29.9	43.8
Control (Path) 3 Hippo	4.6	5.2	5.3
AD 1 Temporal Ctx	12.9	12.8	9.0
AD 2 Temporal Ctx	31.0	45.1	21.0
AD 3 Temporal Ctx	6.0	4.1	3.9
AD 4 Temporal Ctx	20.2	6.8	7.7
AD 5 Inf Temporal Ctx	39.2	1.6	23.7
AD 5 Sup Temporal Ctx	42.0	33.2	11.4

AD 6 Inf Temporal Ctx	49.3	52.1	88.9
AD 6 Sup Temporal Ctx	48.3	37.6	61.1
Control 1 Temporal Ctx	12.9	6.7	2.8
Control 2 Temporal Ctx	18.2	7.3	16.0
Control 3 Temporal Ctx	9.6	4.4	3.1
Control 3 Temporal Ctx	15.2	11.7	13.6
Control (Path) 1 Temporal Ctx	27.0	24.8	13.8
Control (Path) 2 Temporal Ctx	16.0	9.8	2.6
Control (Path) 3 Temporal Ctx	7.5	3.5	6.3
Control (Path) 4 Temporal Ctx	17.1	14.8	7.0
AD 1 Occipital Ctx	10.2	15.0	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	6.4	8.0	0.0
AD 4 Occipital Ctx	13.0	6.8	3.5
AD 5 Occipital Ctx	25.3	12.7	3.8
AD 6 Occipital Ctx	20.2	5.9	8.5
Control 1 Occipital Ctx	6.0	4.1	1.3
Control 2 Occipital Ctx	26.4	20.3	13.7
Control 3 Occipital Ctx	10.7	7.5	5.0
Control 4 Occipital Ctx	12.0	3.3	1.3
Control (Path) 1 Occipital Ctx	35.6	25.9	12.1
Control (Path) 2 Occipital Ctx	6.7	7.4	13.2
Control (Path) 3 Occipital Ctx	5.4	2.3	9.4

Control (Path) 4 Occipital Ctx	13.2	21.0	20.4
Control 1 Parietal Ctx	8.8	12.5	5.0
Control 2 Parietal Ctx	34.4	41.2	25.5
Control 3 Parietal Ctx	11.5	13.2	16.7
Control (Path) 1 Parietal Ctx	34.2	22.5	4.2
Control (Path) 2 Parietal Ctx	19.6	26.8	14.4
Control (Path) 3 Parietal Ctx	3.9	7.5	5.9
Control (Path) 4 Parietal Ctx	24.8	20.6	9.4

Table AVG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6435, Run 277223167	Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6435, Run 277223167
Adipose	2.6	20.0	13.2	Renal ca. TK-10	0.4	3.1	0.7
Melanoma* Hs688(A).T	0.0	2.0	0.9	Bladder	0.0	5.9	6.6
Melanoma* Hs688(B).T	0.2	4.1	1.9	Gastric ca. (liver met.) NCI-N87	0.0	1.7	0.0
Melanoma* M14	0.0	0.7	0.0	Gastric ca. KATO III	0.5	0.8	0.3
Melanoma* LOXIMVI	0.0	0.1	0.0	Colon ca. SW-948	1.5	0.2	0.0
Melanoma* SK-MEL-5	2.2	30.4	4.4	Colon ca. SW480	5.2	41.8	4.4
Squamous cell carcinoma SCC-4	0.0	0.1	0.0	Colon ca.* (SW480 met) SW620	4.8	16.4	1.7
Testis Pool	3.5	8.8	10.0	Colon ca. HT29	0.0	0.0	0.0

Prostate ca.* (bone met) PC-3	0.5	2.5	1.8	Colon ca. HCT-116	0.2	3.2	0.5
Prostate Pool	1.0	11.5	10.0	Colon ca. CaCo-2	3.6	27.0	7.6
Placenta	0.0	0.7	0.3	Colon cancer tissue	3.3	11.0	5.6
Uterus Pool	1.5	4.5	16.2	Colon ca. SW1116	3.0	2.5	1.1
Ovarian ca. OVCAR-3	0.3	1.1	0.4	Colon ca. Colo-205	0.4	0.3	0.0
Ovarian ca. SK-OV-3	0.2	1.7	0.9	Colon ca. SW-48	3.6	1.4	0.0
Ovarian ca. OVCAR-4	0.0	0.9	0.0	Colon Pool	5.0	28.1	44.8
Ovarian ca. OVCAR-5	1.3	2.9	0.3	Small Intestine Pool	1.7	17.1	26.8
Ovarian ca. IGROV-1	**100.0**	77.9	27.0	Stomach Pool	2.3	14.3	24.0
Ovarian ca. OVCAR-8	21.9	14.0	7.6	Bone Marrow Pool	1.6	14.3	25.9
Ovary	0.3	5.2	4.5	Fetal Heart	2.3	25.5	31.6
Breast ca. MCF-7	0.0	0.3	0.0	Heart Pool	7.0	29.7	23.5
Breast ca. MDA-MB-231	0.0	0.4	0.0	Lymph Node Pool	6.1	33.7	64.6
Breast ca. BT 549	0.0	0.5	0.0	Fetal Skeletal Muscle	5.2	54.3	46.7
Breast ca. T47D	0.0	0.5	0.0	Skeletal Muscle Pool	9.2	29.3	24.7
Breast ca. MDA-N	0.0	0.7	0.7	Spleen Pool	0.0	1.9	2.4
Breast Pool	4.1	21.8	42.9	Thymus Pool	2.0	10.4	18.4
Trachea	0.7	8.4	8.3	CNS cancer (glio/astro) U87-MG	1.5	14.9	5.8
Lung	0.7	2.3	3.9	CNS cancer (glio/astro) U-118-MG	0.3	4.7	1.5

Fetal Lung	0.3	9.1	8.0	CNS cancer (neuro;met) SK-N-AS	0.0	2.6	0.7
Lung ca. NCI-N417	0.9	3.5	0.2	CNS cancer (astro) SF-539	0.0	0.0	0.2
Lung ca. LX-1	2.7	6.5	0.9	CNS cancer (astro) SNB-75	1.1	14.9	3.1
Lung ca. NCI-H146	0.0	0.3	0.0	CNS cancer (glio) SNB-19	79.0	**100.0**	12.8
Lung ca. SHP-77	0.4	6.8	0.2	CNS cancer (glio) SF-295	0.0	11.3	0.0
Lung ca. A549	2.6	0.9	0.0	Brain (Amygdala) Pool	0.8	7.7	7.9
Lung ca. NCI-H526	0.0	0.9	0.0	Brain (cerebellum)	0.4	19.8	1.8
Lung ca. NCI-H23	1.0	4.6	0.6	Brain (fetal)	0.7	12.7	8.4
Lung ca. NCI-H460	0.0	0.2	0.0	Brain (Hippocampus) Pool	3.2	11.7	9.9
Lung ca. HOP-62	0.0	0.5	0.0	Cerebral Cortex Pool	0.6	11.0	1.8
Lung ca. NCI-H522	0.6	2.3	0.0	Brain (Substantia nigra) Pool	2.2	11.7	4.2
Liver	0.0	0.0	0.0	Brain (Thalamus) Pool	2.7	13.2	9.1
Fetal Liver	0.3	1.1	0.3	Brain (whole)	0.4	10.6	3.3
Liver ca. HepG2	0.3	0.2	0.0	Spinal Cord Pool	2.3	14.7	13.1
Kidney Pool	0.0	47.0	**100.0**	Adrenal Gland	0.3	9.9	7.4
Fetal Kidney	0.0	4.9	12.1	Pituitary gland Pool	0.0	1.1	1.8
Renal ca. 786-0	0.0	0.2	0.0	Salivary Gland	0.0	1.8	2.3
Renal ca. A498	1.8	0.2	0.0	Thyroid (female)	0.3	3.1	3.3

Renal ca. ACHN	0.5	2.5	0.0	Pancreatic ca. CAPAN2	0.0	0.8	0.5
Renal ca. UO-31	0.0	0.5	0.0	Pancreas Pool	0.0	2.0	3.5

Table AVH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	1.3	0.0	0.0
Secondary Th2 act	0.0	1.2	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.7	0.0
Secondary Tr1 rest	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.7	0.0
Primary Tr1 act	0.0	0.7	0.0	0.0
Primary Th1 rest	0.0	0.1	0.0	0.0
Primary Th2 rest	0.0	0.4	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.8	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	1.6	0.0
CD8 lymphocyte act	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0	0.0
CD4 lymphocyte none	0.0	0.5	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	0.0
LAK cells rest	2.7	11.8	6.1	0.0

LAK cells IL-2	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	6.1	0.0
NK Cells IL-2 rest	0.0	3.4	0.0	0.0
Two Way MLR 3 day	0.0	2.2	0.9	0.0
Two Way MLR 5 day	0.0	0.8	0.0	0.0
Two Way MLR 7 day	13.2	1.1	2.9	0.0
PBMC rest	0.0	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0	0.0
PBMC PHA-L	0.0	0.6	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	9.1	29.1	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	1.0	0.0
Dendritic cells none	13.8	4.1	0.7	0.0
Dendritic cells LPS	0.0	1.0	0.0	0.0
Dendritic cells anti-CD40	3.3	0.5	1.6	0.0
Monocytes rest	0.0	0.4	0.0	0.0
Monocytes LPS	0.0	5.7	0.0	0.4
Macrophages rest	0.0	0.6	0.0	0.0
Macrophages LPS	0.0	5.4	0.8	0.0
HUVEC none	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0

HUVEC TNF alpha + IFN gamma	0.0	0.0	0.6	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0	0.0
Lung Microvascular EC none	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.5	0.3
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0	0.0
Astrocytes rest	**100.0**	**100.0**	**100.0**	54.3
Astrocytes TNFalpha + IL-1beta	74.2	97.3	97.9	**100.0**
KU-812 (Basophil) rest	0.0	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	5.1	0.6
NCI-H292 none	0.0	1.7	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0	0.0
NCI-H292 IL-13	0.0	0.9	0.0	0.0

NCI-H292 IFN gamma	0.0	0.5	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	62.9	26.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	25.2	28.3
Lung fibroblast IL-4	19.1	27.4	23.3	16.0
Lung fibroblast IL-9	23.5	24.0	20.4	9.3
Lung fibroblast IL-13	4.5	11.9	15.0	4.3
Lung fibroblast IFN gamma	15.7	55.9	29.9	25.2
Dermal fibroblast CCD1070 rest	0.0	6.0	5.6	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.8	1.1
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.7	1.6
Dermal fibroblast IFN gamma	8.5	30.6	20.0	4.9
Dermal fibroblast IL-4	4.1	30.8	22.7	13.5
Dermal Fibroblasts rest	8.0	54.3	20.7	15.8
Neutrophils TNFa+LPS	0.0	0.9	1.2	0.0
Neutrophils rest	0.0	0.0	0.0	0.0
Colon	4.0	4.6	7.9	4.8
Lung	0.0	2.8	1.6	0.0
Thymus	0.0	0.0	2.0	0.0
Kidney	4.9	7.8	10.2	0.6

CNS_neurodegeneration_v1.0 Summary: Ag6428/Ag6435/Ag6447 Three experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this

experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6432, Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag6425// Ag6428/Ag6435 Four experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-30). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6432/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/ Ag6428/Ag6435/Ag6447 Four experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6432 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AW. CG56054-16: Integrin alpha 7-like protein.

Expression of gene CG56054-16 was assessed using the primer-probe sets Ag6427, Ag6434, Ag6435 and Ag6447, described in Tables AWA, AWB, AWC and AWD. Results of the RTQ-PCR runs are shown in Tables AWE, AWF and AWG.

Table AWA. Probe Name Ag6427

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	678
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	679
Reverse	5'-ccctggatgcccatc-3'	15	1391	680

Table AWB. Probe Name Ag6434

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctttgatggtgatgggaa-3'	19	1279	681
Probe	TET-5'-cttcatctaccatgggagcagcctg-3'-TAMRA	25	1301	682
Reverse	5'-gctcgggatgcccac-3'	15	1368	683

Table AWC. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	684
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	685
Reverse	5'-cagggaccgggatga-3'	15	829	686

Table AWD. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	687
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	688
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	689

Table AWE. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6434, Run 269253996	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007	Tissue Name	Rel. Exp.(%) Ag6434, Run 269253996	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	17.3	17.1	18.8	Control (Path) 3 Temporal Ctx	9.2	3.5	6.3
AD 2 Hippo	33.0	27.9	10.4	Control (Path) 4 Temporal Ctx	13.8	14.8	7.0
AD 3 Hippo	3.4	4.8	0.0	AD 1 Occipital Ctx	8.4	15.0	0.0
AD 4 Hippo	9.0	18.3	4.6	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	66.4	46.7	11.0	AD 3 Occipital Ctx	3.8	8.0	0.0
AD 6 Hippo	100.0	100.0	100.0	AD 4 Occipital Ctx	1.4	6.8	3.5
Control 2 Hippo	23.3	8.5	3.1	AD 5 Occipital Ctx	21.3	12.7	3.8
Control 4 Hippo	26.6	29.9	43.8	AD 6 Occipital Ctx	15.5	5.9	8.5
Control (Path) 3 Hippo	7.0	5.2	5.3	Control 1 Occipital Ctx	5.5	4.1	1.3
AD 1 Temporal Ctx	13.7	12.8	9.0	Control 2 Occipital Ctx	33.7	20.3	13.7
AD 2 Temporal Ctx	35.8	45.1	21.0	Control 3 Occipital Ctx	3.0	7.5	5.0
AD 3 Temporal Ctx	7.2	4.1	3.9	Control 4 Occipital Ctx	8.1	3.3	1.3

AD 4 Temporal Ctx	6.7	6.8	7.7	Control (Path) 1 Occipital Ctx	39.0	25.9	12.1
AD 5 Inf Temporal Ctx	21.9	1.6	23.7	Control (Path) 2 Occipital Ctx	4.2	7.4	13.2
AD 5 SupTemporal Ctx	31.6	33.2	11.4	Control (Path) 3 Occipital Ctx	3.2	2.3	9.4
AD 6 Inf Temporal Ctx	52.9	52.1	88.9	Control (Path) 4 Occipital Ctx	9.3	21.0	20.4
AD 6 Sup Temporal Ctx	71.2	37.6	61.1	Control 1 Parietal Ctx	10.1	12.5	5.0
Control 1 Temporal Ctx	10.3	6.7	2.8	Control 2 Parietal Ctx	43.5	41.2	25.5
Control 2 Temporal Ctx	16.2	7.3	16.0	Control 3 Parietal Ctx	15.9	13.2	16.7
Control 3 Temporal Ctx	8.5	4.4	3.1	Control (Path) 1 Parietal Ctx	24.8	22.5	4.2
Control 4 Temporal Ctx	13.6	11.7	13.6	Control (Path) 2 Parietal Ctx	22.1	26.8	14.4
Control (Path) 1 Temporal Ctx	29.9	24.8	13.8	Control (Path) 3 Parietal Ctx	9.3	7.5	5.9
Control (Path) 2 Temporal Ctx	13.2	9.8	2.6	Control (Path) 4 Parietal Ctx	34.6	20.6	9.4

Table AWF. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6434, Run 277222451	Rel. Exp.(%) Ag6435, Run 277223167	Tissue Name	Rel. Exp.(%) Ag6434, Run 277222451	Rel. Exp.(%) Ag6435, Run 277223167
Adipose	9.5	13.2	Renal ca. TK-10	3.0	0.7

Melanoma* Hs688(A).T	0.9	0.9	Bladder	3.4	6.6
Melanoma* Hs688(B).T	3.7	1.9	Gastric ca. (liver met.) NCI-N87	1.1	0.0
Melanoma* M14	0.7	0.0	Gastric ca. KATO III	0.0	0.3
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW-948	0.0	0.0
Melanoma* SK-MEL-5	14.7	4.4	Colon ca. SW480	28.3	4.4
Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	11.7	1.7
Testis Pool	5.7	10.0	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	1.5	1.8	Colon ca. HCT-116	5.0	0.5
Prostate Pool	4.2	10.0	Colon ca. CaCo-2	14.9	7.6
Placenta	0.5	0.3	Colon cancer tissue	9.2	5.6
Uterus Pool	2.5	16.2	Colon ca. SW1116	2.2	1.1
Ovarian ca. OVCAR-3	0.8	0.4	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	0.8	0.9	Colon ca. SW-48	1.4	0.0
Ovarian ca. OVCAR-4	0.5	0.0	Colon Pool	14.2	44.8
Ovarian ca. OVCAR-5	2.9	0.3	Small Intestine Pool	7.4	26.8
Ovarian ca. IGROV-1	73.7	27.0	Stomach Pool	9.2	24.0
Ovarian ca. OVCAR-8	20.7	7.6	Bone Marrow Pool	4.6	25.9
Ovary	4.0	4.5	Fetal Heart	11.3	31.6
Breast ca. MCF-7	0.5	0.0	Heart Pool	15.2	23.5
Breast ca. MDA-MB-231	0.5	0.0	Lymph Node Pool	14.1	64.6
Breast ca. BT 549	0.5	0.0	Fetal Skeletal Muscle	33.0	46.7
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	21.2	24.7

Breast ca. MDA-N	0.0	0.7	Spleen Pool	1.2	2.4
Breast Pool	9.6	42.9	Thymus Pool	6.1	18.4
Trachea	5.3	8.3	CNS cancer (glio/astro) U87-MG	10.4	5.8
Lung	1.3	3.9	CNS cancer (glio/astro) U-118-MG	3.4	1.5
Fetal Lung	5.0	8.0	CNS cancer (neuro;met) SK-N-AS	1.8	0.7
Lung ca. NCI-N417	3.0	0.2	CNS cancer (astro) SF-539	0.0	0.2
Lung ca. LX-1	4.3	0.9	CNS cancer (astro) SNB-75	12.0	3.1
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	**100.0**	12.8
Lung ca. SHP-77	4.9	0.2	CNS cancer (glio) SF-295	7.7	0.0
Lung ca. A549	0.7	0.0	Brain (Amygdala) Pool	5.5	7.9
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	11.0	1.8
Lung ca. NCI-H23	3.1	0.6	Brain (fetal)	6.9	8.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	8.5	9.9
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	6.8	1.8
Lung ca. NCI-H522	1.4	0.0	Brain (Substantia nigra) Pool	5.2	4.2
Liver	0.0	0.0	Brain (Thalamus) Pool	6.8	9.1
Fetal Liver	0.5	0.3	Brain (whole)	6.8	3.3
Liver ca. HepG2	0.5	0.0	Spinal Cord Pool	6.4	13.1
Kidney Pool	22.8	**100.0**	Adrenal Gland	8.4	7.4
Fetal Kidney	2.4	12.1	Pituitary gland Pool	0.6	1.8
Renal ca. 786-0	0.0	0.0	Salivary Gland	1.6	2.3

Renal ca. A498	0.0	0.0	Thyroid (female)	2.6	3.3
Renal ca. ACHN	0.7	0.0	Pancreatic ca. CAPAN2	0.9	0.5
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.8	3.5

Table AWG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6434, Run 268713326	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806	Tissue Name	Rel. Exp.(%) Ag6434, Run 268713326	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	0.0	0.0	HUVEC IL-1beta	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0	HUVEC IFN gamma	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0
Secondary Th1 rest	0.0	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0	HUVEC IL-11	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	Lung Microvascular EC none	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0	Microvascular Dermal EC none	0.0	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Primary Th2 rest	0.0	0.0	0.0	Small airway epithelium none	0.0	0.0	0.0

Primary Tr1 rest	0.0	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	0.0	Coronery artery SMC rest	0.0	0.5	0.3
CD45RO CD4 lymphocyte act	3.9	1.6	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0	0.0
CD8 lymphocyte act	0.0	0.0	0.0	Astrocytes rest	**100.0**	**100.0**	54.3
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	Astrocytes TNFalpha + IL-1beta	97.3	97.9	**100.0**
Secondary CD8 lymphocyte act	0.0	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	CCD1106 (Keratinocytes) none	0.0	0.0	0.0
LAK cells rest	7.9	6.1	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
LAK cells IL-2	0.0	0.0	0.0	Liver cirrhosis	3.4	5.1	0.6
LAK cells IL-2+IL-12	0.0	0.0	0.0	NCI-H292 none	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	NCI-H292 IL-4	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	NCI-H292 IL-9	0.0	0.0	0.0
LAK cells PMA/ionomycin	7.0	6.1	0.0	NCI-H292 IL-13	0.0	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0	0.0
Two Way MLR 3 day	0.0	0.9	0.0	HPAEC none	0.0	0.0	0.0
Two Way MLR 5 day	0.0	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0

Two Way MLR 7 day	0.0	2.9	0.0	Lung fibroblast none	72.7	62.9	26.2
PBMC rest	0.0	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	36.6	25.2	28.3
PBMC PWM	0.0	0.0	0.0	Lung fibroblast IL-4	62.4	23.3	16.0
PBMC PHA-L	0.0	0.0	0.0	Lung fibroblast IL-9	52.5	20.4	9.3
Ramos (B cell) none	0.0	0.0	0.0	Lung fibroblast IL-13	14.6	15.0	4.3
Ramos (B cell) ionomycin	0.0	0.0	0.0	Lung fibroblast IFN gamma	41.5	29.9	25.2
B lymphocytes PWM	0.0	0.0	0.0	Dermal fibroblast CCD1070 rest	5.1	5.6	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	7.2	0.8	1.1
EOL-1 dbcAMP	4.4	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	1.6
EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	0.0	Dermal fibroblast IFN gamma	24.5	20.0	4.9
Dendritic cells none	4.5	0.7	0.0	Dermal fibroblast IL-4	28.7	22.7	13.5
Dendritic cells LPS	0.0	0.0	0.0	Dermal Fibroblasts rest	44.4	20.7	15.8
Dendritic cells anti-CD40	0.0	1.6	0.0	Neutrophils TNFa+LPS	0.0	1.2	0.0
Monocytes rest	0.0	0.0	0.0	Neutrophils rest	0.0	0.0	0.0
Monocytes LPS	5.9	0.0	0.4	Colon	4.1	7.9	4.8
Macrophages rest	0.0	0.0	0.0	Lung	0.0	1.6	0.0
Macrophages LPS	9.1	0.8	0.0	Thymus	0.0	2.0	0.0
HUVEC none	0.0	0.0	0.0	Kidney	8.1	10.2	0.6
HUVEC starved	0.0	0.0	0.0				

CNS_neurodegeneration_v1.0 Summary: Ag6434/Ag6435/Ag6447 Three experiments with different probe and primer sets are in good agreements. This panel

confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6427 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag6434 Highest expression of this gene is detected in a brain cancer SNB-19 cell lines (CT=31.9). In addition, moderate to low levels of expression of this gene is also seen in some of the colon, ovarian and brain cancer cell lines. Thus, expression of this gene may be used as a marker to detect the presence of colon, ovarian and brain cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of these cancers.

Ag6435 Highest expression of this gene is detected in kidney (CT=30.6). Moderate levels of expression of this gene is seen in normal tissues represented by breast, testis, prostate, uterus, gastrointestinal tract, and tissues with metabolic/endocrine functions including adipose, heart, skeletal muscle, and adernal gland. Therefore, therapeutic modulation of this gene or its protein product may be useful in the treatment of diseases associated with these tissues, including obesity, diabetes and inflammatory bowel disease. In addition, moderate to low levels of expression of this gene is also seen in some regions of central nervous system, and some brain, colon and ovarian cancer cell lines.

Ag6427/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6434/Ag6435/Ag6447 Three experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.8). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these

cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6427 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AX. CG56054-17: Integrin alpha 7-like protein.

Expression of gene CG56054-17 was assessed using the primer-probe sets Ag6425, Ag6426, Ag6435, Ag6439, Ag6440 and Ag6447, described in Tables AXA, AXB, AXC, AXD, AXE and AXF. Results of the RTQ-PCR runs are shown in Tables AXG, AXH and AXI.

Table AXA. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1499	690
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1531	691
Reverse	5'-gccctggatgcccat-3'	15	1550	692

Table AXB. Probe Name Ag6426

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtcactgggctgggatct-3'	18	1156	693
Probe	TET-5'-ctctccggctctgcggctc-3'-TAMRA	19	1177	694
Reverse	5'-actccttctgccaccaca-3'	18	1254	695

Table AXC. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	696
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	697
Reverse	5'-cagggaccgggatga-3'	15	829	698

Table AXD. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1253	699
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1273	700
Reverse	5'-gaagaatcccatcttccacag-3'	21	1339	701

Table AXE. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1456	702
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	1523	703
Reverse	5'-ccctggatgcccatc-3'	15	1549	704

Table AXF. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	705
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	706
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	707

Table AXG. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	24.1	17.1	21.6	18.9	18.8
AD 2 Hippo	48.0	27.9	28.9	61.1	10.4
AD 3 Hippo	6.5	4.8	6.1	9.7	0.0
AD 4 Hippo	13.8	18.3	17.6	23.3	4.6
AD 5 Hippo	52.9	46.7	42.6	34.6	11.0
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0

Control 2 Hippo	10.6	8.5	32.5	29.9	3.1
Control 4 Hippo	51.8	29.9	37.9	54.7	43.8
Control (Path) 3 Hippo	9.8	5.2	6.4	5.8	5.3
AD 1 Temporal Ctx	10.1	12.8	24.5	12.6	9.0
AD 2 Temporal Ctx	33.7	45.1	27.5	59.0	21.0
AD 3 Temporal Ctx	0.0	4.1	9.0	17.1	3.9
AD 4 Temporal Ctx	12.8	6.8	30.4	29.9	7.7
AD 5 Inf Temporal Ctx	59.0	1.6	41.8	41.8	23.7
AD 5 Sup Temporal Ctx	21.9	33.2	38.7	39.2	11.4
AD 6 Inf Temporal Ctx	73.7	52.1	47.6	48.6	88.9
AD 6 Sup Temporal Ctx	50.3	37.6	50.3	17.0	61.1
Control 1 Temporal Ctx	11.9	6.7	24.0	23.3	2.8
Control 2 Temporal Ctx	18.6	7.3	14.9	43.5	16.0
Control 3 Temporal Ctx	6.0	4.4	16.5	9.2	3.1
Control 3 Temporal Ctx	25.7	11.7	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	18.0	24.8	39.8	51.1	13.8
Control (Path) 2 Temporal Ctx	18.4	9.8	24.8	7.2	2.6
Control (Path) 3 Temporal Ctx	5.6	3.5	11.9	9.9	6.3
Control (Path) 4 Temporal Ctx	16.8	14.8	21.6	14.9	7.0
AD 1 Occipital Ctx	11.9	15.0	16.0	5.8	0.0

AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	8.3	8.0	10.2	7.8	0.0
AD 4 Occipital Ctx	5.8	6.8	18.6	35.4	3.5
AD 5 Occipital Ctx	25.2	12.7	22.7	16.6	3.8
AD 6 Occipital Ctx	19.8	5.9	22.1	23.5	8.5
Control 1 Occipital Ctx	6.6	4.1	7.2	15.2	1.3
Control 2 Occipital Ctx	15.7	20.3	29.3	35.8	13.7
Control 3 Occipital Ctx	5.7	7.5	19.2	4.4	5.0
Control 4 Occipital Ctx	21.6	3.3	13.6	12.9	1.3
Control (Path) 1 Occipital Ctx	28.3	25.9	39.5	22.4	12.1
Control (Path) 2 Occipital Ctx	49.7	7.4	7.0	5.0	13.2
Control (Path) 3 Occipital Ctx	0.0	2.3	5.9	6.7	9.4
Control (Path) 4 Occipital Ctx	6.6	21.0	11.4	11.9	20.4
Control 1 Parietal Ctx	8.8	12.5	15.7	33.2	5.0
Control 2 Parietal Ctx	14.5	41.2	37.1	17.4	25.5
Control 3 Parietal Ctx	19.9	13.2	10.8	21.6	16.7
Control (Path) 1 Parietal Ctx	37.6	22.5	37.9	47.3	4.2
Control (Path) 2 Parietal Ctx	16.6	26.8	18.7	17.1	14.4
Control (Path) 3 Parietal Ctx	0.0	7.5	12.0	11.7	5.9

Control (Path) 4 Parietal Ctx	18.2	20.6	27.9	29.3	9.4

Table AXH. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	2.6	13.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.9	0.4	0.0
Melanoma* Hs688(B).T	0.2	1.9	2.9	0.8
Melanoma* M14	0.0	0.0	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	2.2	4.4	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.0
Testis Pool	3.5	10.0	9.1	3.0
Prostate ca.* (bone met) PC-3	0.5	1.8	1.3	1.2
Prostate Pool	1.0	10.0	28.5	2.1
Placenta	0.0	0.3	0.5	0.0
Uterus Pool	1.5	16.2	5.3	2.3
Ovarian ca. OVCAR-3	0.3	0.4	1.6	0.4
Ovarian ca. SK-OV-3	0.2	0.9	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.0
Ovarian ca. OVCAR-5	1.3	0.3	1.4	4.2
Ovarian ca. IGROV-1	**100.0**	27.0	69.3	**100.0**
Ovarian ca. OVCAR-8	21.9	7.6	17.3	18.2
Ovary	0.3	4.5	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.6	0.0
Breast ca. T47D	0.0	0.0	0.4	0.3

Breast ca. MDA-N	0.0	0.7	0.6	0.3
Breast Pool	4.1	42.9	12.2	3.5
Trachea	0.7	8.3	4.7	1.4
Lung	0.7	3.9	3.9	5.3
Fetal Lung	0.3	8.0	5.3	2.9
Lung ca. NCI-N417	0.9	0.2	4.0	2.0
Lung ca. LX-1	2.7	0.9	4.9	6.3
Lung ca. NCI-H146	0.0	0.0	0.1	0.0
Lung ca. SHP-77	0.4	0.2	4.5	0.8
Lung ca. A549	2.6	0.0	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.4	0.3
Lung ca. NCI-H23	1.0	0.6	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.5	0.0
Lung ca. NCI-H522	0.6	0.0	3.3	2.5
Liver	0.0	0.0	0.1	0.4
Fetal Liver	0.3	0.3	0.8	0.8
Liver ca. HepG2	0.3	0.0	0.1	0.9
Kidney Pool	0.0	**100.0**	43.2	14.6
Fetal Kidney	0.0	12.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.3	0.0
Renal ca. A498	1.8	0.0	0.5	3.8
Renal ca. ACHN	0.5	0.0	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.6	0.0
Renal ca. TK-10	0.4	0.7	2.1	0.5
Bladder	0.0	6.6	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.1	0.8
Gastric ca. KATO III	0.5	0.3	0.4	0.4
Colon ca. SW-948	1.5	0.0	0.3	2.2
Colon ca. SW480	5.2	4.4	23.0	6.3

Colon ca.* (SW480 met) SW620	4.8	1.7	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.3
Colon ca. HCT-116	0.2	0.5	2.1	0.6
Colon ca. CaCo-2	3.6	7.6	18.3	6.5
Colon cancer tissue	3.3	5.6	7.7	4.4
Colon ca. SW1116	3.0	1.1	1.8	2.1
Colon ca. Colo-205	0.4	0.0	0.2	1.3
Colon ca. SW-48	3.6	0.0	1.4	3.0
Colon Pool	5.0	44.8	25.5	8.1
Small Intestine Pool	1.7	26.8	12.8	2.0
Stomach Pool	2.3	24.0	8.5	4.2
Bone Marrow Pool	1.6	25.9	18.7	3.5
Fetal Heart	2.3	31.6	33.7	8.6
Heart Pool	7.0	23.5	33.7	10.7
Lymph Node Pool	6.1	64.6	19.9	6.7
Fetal Skeletal Muscle	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	9.2	24.7	22.1	22.7
Spleen Pool	0.0	2.4	2.7	0.6
Thymus Pool	2.0	18.4	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.5	5.8	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.3	1.5	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.1	3.1	11.7	2.8
CNS cancer (glio) SNB-19	79.0	12.8	**100.0**	97.9
CNS cancer (glio) SF-295	0.0	0.0	8.2	1.5

Brain (Amygdala) Pool	0.8	7.9	8.0	4.4
Brain (cerebellum)	0.4	1.8	8.8	1.2
Brain (fetal)	0.7	8.4	6.8	2.1
Brain (Hippocampus) Pool	3.2	9.9	11.0	4.3
Cerebral Cortex Pool	0.6	1.8	11.6	2.0
Brain (Substantia nigra) Pool	2.2	4.2	10.0	2.0
Brain (Thalamus) Pool	2.7	9.1	9.7	2.8
Brain (whole)	0.4	3.3	5.6	1.9
Spinal Cord Pool	2.3	13.1	12.2	4.2
Adrenal Gland	0.3	7.4	4.8	0.9
Pituitary gland Pool	0.0	1.8	1.4	0.6
Salivary Gland	0.0	2.3	1.1	0.0
Thyroid (female)	0.3	3.3	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.5	0.7	0.6
Pancreas Pool	0.0	3.5	3.2	1.0

Table AXI. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.0	0.0

Primary Tr1 rest	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.0	1.6	2.3	0.0
CD8 lymphocyte act	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2	0.0
LAK cells rest	2.7	6.1	15.2	0.0
LAK cells IL-2	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	6.1	9.0	0.0
NK Cells IL-2 rest	0.0	0.0	1.4	0.0
Two Way MLR 3 day	0.0	0.9	1.4	0.0
Two Way MLR 5 day	0.0	0.0	0.0	0.0
Two Way MLR 7 day	13.2	2.9	3.7	0.0
PBMC rest	0.0	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.0	68.8	0.0

EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	1.8	0.0
Dendritic cells none	13.8	0.7	0.0	0.0
Dendritic cells LPS	0.0	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	1.6	0.0	0.0
Monocytes rest	0.0	0.0	0.0	0.0
Monocytes LPS	0.0	0.0	2.6	0.4
Macrophages rest	0.0	0.0	0.0	0.0
Macrophages LPS	0.0	0.8	9.2	0.0
HUVEC none	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0	0.0
Astrocytes rest	**100.0**	**100.0**	**100.0**	54.3

Astrocytes TNFalpha + IL-1beta	74.2	97.9	95.9	100.0
KU-812 (Basophil) rest	0.0	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	5.1	8.5	0.6
NCI-H292 none	0.0	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	25.2	62.9	28.3
Lung fibroblast IL-4	19.1	23.3	34.9	16.0
Lung fibroblast IL-9	23.5	20.4	96.6	9.3
Lung fibroblast IL-13	4.5	15.0	13.4	4.3
Lung fibroblast IFN gamma	15.7	29.9	89.5	25.2
Dermal fibroblast CCD1070 rest	0.0	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	0.0	1.6
Dermal fibroblast IFN gamma	8.5	20.0	26.6	4.9
Dermal fibroblast IL-4	4.1	22.7	25.5	13.5
Dermal Fibroblasts rest	8.0	20.7	47.3	15.8

Neutrophils TNFa+LPS	0.0	1.2	0.0	0.0
Neutrophils rest	0.0	0.0	0.0	0.0
Colon	4.0	7.9	8.4	4.8
Lung	0.0	1.6	2.1	0.0
Thymus	0.0	2.0	2.4	0.0
Kidney	4.9	10.2	5.2	0.6

CNS_neurodegeneration_v1.0 Summary: Ag6425/Ag6435/Ag6439/Ag6440/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6426 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag6425/Ag6435/Ag6439/Ag6440 Four experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-30). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6447 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/Ag6435/Ag6439/Ag6447 Four experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6426/ Ag6440 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AY. CG56054-18: Integrin alpha 7-like protein.

Expression of gene CG56054-18 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6428, Ag6431, Ag6435, Ag6439, Ag6447, Ag6413 and Ag6964, described in Tables AYA, AYB, AYC, AYD, AYE, AYF, AYG, AYH, AYI and AYJ. Results of the RTQ-PCR runs are shown in Tables AYK, AYL, AYM, AYN, AYO and AYP.

Table AYA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	708
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	709
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	710

Table AYB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	711
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	712
Reverse	5'-gcgcagtccagggtg-3'	15	2906	713

Table AYC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3296	714
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3328	715
Reverse	5'-gccctggatgcccat-3'	15	3347	716

Table AYD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	717
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	718
Reverse	5'-agggagtagccgaagctct-3'	19	1378	719

Table AYE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	720
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	721
Reverse	5'-ccgcgcggtcaaa-3'	13	2967	722

Table AYF. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	723
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	724
Reverse	5'-cagggaccgggatga-3'	15	829	725

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Table AYG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No

Forward	5'-ctgtggtggcagaaggagt-3'	19	3157	726
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3177	727
Reverse	5'-gaagaatcccatcttccacag-3'	21	3243	728

Table AYH. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	729
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	730
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	731

Table AYI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	732
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	733
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	734

Table AYJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	735
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	736
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	737

Table AYK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	24.1	18.0	18.8	17.1	21.6	19.2	18.8
AD 2 Hippo	41.2	52.9	48.0	32.3	28.7	27.9	28.9	49.7	10.4
AD 3 Hippo	8.9	6.4	6.5	3.7	7.5	4.8	6.1	20.4	0.0
AD 4 Hippo	14.8	25.5	13.8	10.7	18.8	18.3	17.6	5.6	4.6
AD 5 Hippo	44.8	41.8	52.9	53.2	38.4	46.7	42.6	57.4	11.0
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1	**100.0**
Control 2 Hippo	24.3	36.1	10.6	18.7	29.5	8.5	32.5	28.5	3.1
Control 4 Hippo	42.9	43.8	51.8	27.0	32.3	29.9	37.9	86.5	43.8
Control (Path) 3 Hippo	14.2	11.4	9.8	4.6	6.0	5.2	6.4	0.0	5.3
AD 1 Temporal Ctx	23.3	15.9	10.1	12.9	17.1	12.8	24.5	16.8	9.0
AD 2 Temporal Ctx	41.5	47.3	33.7	31.0	39.8	45.1	27.5	21.6	21.0
AD 3 Temporal Ctx	9.5	9.8	0.0	6.0	11.3	4.1	9.0	5.7	3.9
AD 4 Temporal Ctx	30.6	39.0	12.8	20.2	25.3	6.8	30.4	8.7	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	59.0	39.2	36.3	1.6	41.8	73.7	23.7

AD 5 Sup Temporal Ctx	51.1	39.0	21.9	42.0	32.3	33.2	38.7	55.9	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	73.7	49.3	46.7	52.1	47.6	76.8	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	50.3	48.3	50.3	37.6	50.3	59.9	61.1
Control 1 Temporal Ctx	12.2	23.0	11.9	12.9	15.6	6.7	24.0	46.7	2.8
Control 2 Temporal Ctx	14.2	32.5	18.6	18.2	17.4	7.3	14.9	50.0	16.0
Control 3 Temporal Ctx	15.1	15.3	6.0	9.6	14.5	4.4	16.5	9.5	3.1
Control 3 Temporal Ctx	23.7	25.0	25.7	15.2	13.1	11.7	23.8	13.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	18.0	27.0	30.6	24.8	39.8	46.0	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	18.4	16.0	20.4	9.8	24.8	0.0	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	5.6	7.5	10.9	3.5	11.9	31.0	6.3
Control (Path) 4 Temporal Ctx	21.9	27.4	16.8	17.1	18.2	14.8	21.6	39.5	7.0
AD 1 Occipital Ctx	16.0	11.9	11.9	10.2	11.5	15.0	16.0	6.3	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

AD 3 Occipital Ctx	10.7	6.0	8.3	6.4	8.8	8.0	10.2	4.9	0.0
AD 4 Occipital Ctx	18.9	23.7	5.8	13.0	17.9	6.8	18.6	11.1	3.5
AD 5 Occipital Ctx	24.8	28.3	25.2	25.3	22.5	12.7	22.7	42.3	3.8
AD 6 Occipital Ctx	20.6	31.9	19.8	20.2	17.0	5.9	22.1	14.8	8.5
Control 1 Occipital Ctx	9.5	14.4	6.6	6.0	8.7	4.1	7.2	8.8	1.3
Control 2 Occipital Ctx	31.9	42.6	15.7	26.4	33.2	20.3	29.3	82.4	13.7
Control 3 Occipital Ctx	18.8	13.0	5.7	10.7	17.1	7.5	19.2	8.8	5.0
Control 4 Occipital Ctx	18.2	17.0	21.6	12.0	12.6	3.3	13.6	24.0	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	28.3	35.6	36.1	25.9	39.5	**100.0**	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	49.7	6.7	7.9	7.4	7.0	9.3	13.2
Control (Path) 3 Occipital Ctx	4.8	8.7	0.0	5.4	6.0	2.3	5.9	4.1	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	6.6	13.2	10.2	21.0	11.4	32.8	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	8.8	16.3	12.5	15.7	9.2	5.0

Control 2 Parietal Ctx	32.8	28.9	14.5	34.4	28.3	41.2	37.1	28.1	25.5
Control 3 Parietal Ctx	20.6	19.8	19.9	11.5	8.7	13.2	10.8	9.1	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	37.6	34.2	39.2	22.5	37.9	69.3	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	16.6	19.6	22.5	26.8	18.7	37.6	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	0.0	3.9	7.1	7.5	12.0	10.4	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	18.2	24.8	8.8	20.6	27.9	27.5	9.4

Table AYL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8

Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9

Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AYM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3

Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0

Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AYN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	20.0	17.4	13.8	13.2	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.8	0.9	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.2	4.1	2.5	2.2	1.9	2.9	2.4
Melanoma* M14	0.3	0.0	0.7	0.4	0.4	0.0	0.4	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	2.2	30.4	18.2	14.6	4.4	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	3.5	8.8	10.4	9.0	10.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	2.5	1.9	1.8	1.8	1.3	4.3
Prostate Pool	8.1	1.0	11.5	11.3	12.1	10.0	28.5	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.3	0.5	0.4
Uterus Pool	2.2	1.5	4.5	4.6	4.5	16.2	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.3	1.1	0.7	1.1	0.4	1.6	4.0

Ovarian ca. SK-OV-3	0.8	0.2	1.7	0.8	0.9	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.4	0.8	0.0	0.9	0.5
Ovarian ca. OVCAR-5	1.6	1.3	2.9	1.3	1.7	0.3	1.4	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	77.9	84.7	97.9	27.0	69.3	75.8
Ovarian ca. OVCAR-8	13.6	21.9	14.0	15.6	14.6	7.6	17.3	16.7
Ovary	2.7	0.3	5.2	3.1	2.3	4.5	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.1	0.2	0.0	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.4	0.2	0.2	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.1	0.5	0.0	0.6	0.4
Breast ca. T47D	0.0	0.0	0.5	0.2	0.3	0.0	0.4	0.5
Breast ca. MDA-N	0.6	0.0	0.7	0.6	0.6	0.7	0.6	0.8
Breast Pool	15.0	4.1	21.8	14.6	10.7	42.9	12.2	16.7
Trachea	4.5	0.7	8.4	4.8	4.2	8.3	4.7	5.6
Lung	2.8	0.7	2.3	4.2	3.2	3.9	3.9	5.1
Fetal Lung	3.9	0.3	9.1	5.0	4.8	8.0	5.3	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	3.3	2.6	0.2	4.0	2.3
Lung ca. LX-1	3.5	2.7	6.5	5.0	3.5	0.9	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	0.4	6.8	5.3	4.5	0.2	4.5	3.8
Lung ca. A549	0.3	2.6	0.9	0.0	0.4	0.0	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.6	0.3	0.0	0.4	0.5

Lung ca. NCI-H23	2.9	1.0	4.6	4.8	3.2	0.6	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.5	1.0	0.6	0.0	0.5	0.7
Lung ca. NCI-H522	1.7	0.6	2.3	1.7	1.3	0.0	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.3	1.1	0.6	0.5	0.3	0.8	8.2
Liver ca. HepG2	0.1	0.3	0.2	0.0	0.2	0.0	0.1	2.4
Kidney Pool	27.9	0.0	47.0	33.9	28.1	**100.0**	43.2	32.8
Fetal Kidney	1.4	0.0	4.9	4.1	4.0	12.1	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.3	0.1	0.0	0.3	0.9
Renal ca. A498	0.0	1.8	0.2	0.0	0.3	0.0	0.5	8.5
Renal ca. ACHN	1.5	0.5	2.5	1.7	1.5	0.0	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.2	0.2	0.0	0.6	0.3
Renal ca. TK-10	1.9	0.4	3.1	2.0	1.9	0.7	2.1	4.6
Bladder	4.2	0.0	5.9	5.5	5.1	6.6	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	0.9	1.2	0.0	1.1	6.7
Gastric ca. KATO III	0.4	0.5	0.8	0.2	0.3	0.3	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.2	0.0	0.3	1.2
Colon ca. SW480	20.9	5.2	41.8	27.0	23.3	4.4	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	4.8	16.4	12.8	10.3	1.7	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.2	0.2	0.0	0.0	0.3

Colon ca. HCT-116	2.1	0.2	3.2	2.5	2.0	0.5	2.1	4.3
Colon ca. CaCo-2	15.0	3.6	27.0	19.1	16.7	7.6	18.3	38.2
Colon cancer tissue	9.0	3.3	11.0	11.9	7.6	5.6	7.7	20.4
Colon ca. SW1116	1.3	3.0	2.5	2.0	1.5	1.1	1.8	6.0
Colon ca. Colo-205	0.1	0.4	0.3	0.2	0.0	0.0	0.2	0.8
Colon ca. SW-48	0.8	3.6	1.4	1.5	1.5	0.0	1.4	2.6
Colon Pool	20.3	5.0	28.1	23.2	18.7	44.8	25.5	20.6
Small Intestine Pool	14.0	1.7	17.1	11.2	13.0	26.8	12.8	10.4
Stomach Pool	8.1	2.3	14.3	9.5	9.3	24.0	8.5	10.7
Bone Marrow Pool	6.8	1.6	14.3	10.2	8.7	25.9	18.7	12.5
Fetal Heart	10.1	2.3	25.5	24.5	21.8	31.6	33.7	20.7
Heart Pool	28.7	7.0	29.7	25.9	17.2	23.5	33.7	26.1
Lymph Node Pool	17.6	6.1	33.7	22.1	23.7	64.6	19.9	24.7
Fetal Skeletal Muscle	31.9	5.2	54.3	48.6	46.3	46.7	19.1	50.7
Skeletal Muscle Pool	17.4	9.2	29.3	29.5	25.9	24.7	22.1	32.3
Spleen Pool	0.9	0.0	1.9	2.0	1.7	2.4	2.7	3.1
Thymus Pool	4.4	2.0	10.4	8.1	9.4	18.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	14.9	10.7	10.0	5.8	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	4.7	3.8	3.1	1.5	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	2.1	1.0	0.7	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.1	0.2	0.2	0.1	0.1

CNS cancer (astro) SNB-75	8.1	1.1	14.9	6.5	10.0	3.1	11.7	9.7
CNS cancer (glio) SNB-19	79.6	79.0	**100.0**	**100.0**	**100.0**	12.8	**100.0**	**100.0**
CNS cancer (glio) SF-295	8.2	0.0	11.3	8.0	7.8	0.0	8.2	14.8
Brain (Amygdala) Pool	3.7	0.8	7.7	6.2	4.8	7.9	8.0	5.3
Brain (cerebellum)	12.0	0.4	19.8	10.7	9.7	1.8	8.8	9.7
Brain (fetal)	4.2	0.7	12.7	6.6	5.6	8.4	6.8	6.4
Brain (Hippocampus) Pool	7.5	3.2	11.7	8.6	6.9	9.9	11.0	10.2
Cerebral Cortex Pool	9.7	0.6	11.0	7.5	0.7	1.8	11.6	8.7
Brain (Substantia nigra) Pool	7.4	2.2	11.7	10.4	4.7	4.2	10.0	9.3
Brain (Thalamus) Pool	7.6	2.7	13.2	9.3	0.2	9.1	9.7	8.7
Brain (whole)	6.1	0.4	10.6	5.8	0.3	3.3	5.6	8.7
Spinal Cord Pool	10.1	2.3	14.7	11.0	7.6	13.1	12.2	9.0
Adrenal Gland	3.5	0.3	9.9	3.9	3.7	7.4	4.8	4.1
Pituitary gland Pool	0.9	0.0	1.1	1.2	1.1	1.8	1.4	0.5
Salivary Gland	0.9	0.0	1.8	1.3	0.9	2.3	1.1	1.0
Thyroid (female)	2.0	0.3	3.1	2.5	2.5	3.3	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.8	0.7	0.6	0.5	0.7	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.6	3.5	3.2	2.3

Table AYO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	1.6	2.3	0.0
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0	0.0	0.0

2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0	1.2	0.0
LAK cells rest	5.6	5.0	2.7	11.8	3.8	6.1	15.2	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	6.3	6.1	9.0	0.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	0.0	1.4	0.0
Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	0.9	1.4	0.0
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.0	0.0	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	2.9	3.7	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	0.0	68.8	0.0

EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.0	1.8	0.0
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	0.7	0.0	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	0.0	0.0	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	1.6	0.0	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	0.0	2.6	0.4
Macrophages rest	0.9	1.8	0.0	0.6	0.6	0.0	0.0	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	0.8	9.2	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	1.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	54.3
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	74.2	97.3	74.7	97.9	95.9	**100.0**
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	5.1	8.5	0.6
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0	0.0	0.0

NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0	0.0	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	25.2	62.9	28.3
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	23.3	34.9	16.0
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	20.4	96.6	9.3
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	15.0	13.4	4.3
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	29.9	89.5	25.2
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	20.0	26.6	4.9
Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	22.7	25.5	13.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	20.7	47.3	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	1.2	0.0	0.0

Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0	0.0	0.0
Colon	7.9	4.7	4.0	4.6	9.5	7.9	8.4	4.8
Lung	2.2	1.2	0.0	2.8	4.6	1.6	2.1	0.0
Thymus	3.1	0.8	0.0	0.0	0.4	2.0	2.4	0.0
Kidney	4.2	4.4	4.9	7.8	9.7	10.2	5.2	0.6

Table AYP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	100.0	100.0	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2

Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/ Ag6425/Ag6428/Ag6431/ Ag6435/Ag6439/Ag6442/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

Summary: Ag6413/Ag6425/Ag6428/Ag6431/Ag6435/Ag6439/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6442 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D

Summary: Ag4983/Ag6425/Ag6428/Ag6431/Ag6435/Ag6439/Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a

functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AZ. CG56054-19: Integrin alpha 7-like protein.

Expression of gene CG56054-19 was assessed using the primer-probe sets Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6439, Ag6440, Ag6391 and Ag6964, described in Tables AZA, AZB, AZC, AZD, AZE, AZF, AZG, AZH, AZI and AZJ. Results of the RTQ-PCR runs are shown in Tables AZK, AZL, AZM, AZN and AZO.

Table AZA. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	1951	738
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	1990	739
Reverse	5'-gcgcagtccagggtg-3'	15	2076	740

Table AZB. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	641	741
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	660	742
Reverse	5'-aaaagcaacccctccaa-3'	18	723	743

Table AZC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	2573	744
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	2605	745
Reverse	5'-gccctggatgcccat-3'	15	2624	746

Table AZD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1293	747
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1333	748
Reverse	5'-agggagtagccgaagctct-3'	19	1370	749

Table AZE. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	742	750
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	765	751
Reverse	5'-gggagccggtcagca-3'	15	798	752

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Table AZF. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2070	753
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2111	754
Reverse	5'-ccgcgcggtcaaa-3'	13	2137	755

Table AZG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	2327	756
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	2347	757
Reverse	5'-gaagaatcccatcttccacag-3'	21	2413	758

Table AZH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	2530	759
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	2597	760
Reverse	5'-ccctggatgcccatc-3'	15	2623	761

Table AZI. Probe Name Ag6391

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tgcctccagggcctg-3'	15	1892	762
Probe	TET-5'-ctcccaggcccaacatcctcca-3'-TAMRA	22	1925	763
Reverse	5'-cgcctcctatccctactgtc-3'	20	1957	764

Table AZJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2156	765

Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2127	766
Reverse	5'-gccaactgtgtggtgttca-3'	19	2101	767

Table AZK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	24.1	18.0	20.0	18.8	21.6	18.9	19.2
AD 2 Hippo	48.0	32.3	48.0	28.7	28.9	61.1	49.7
AD 3 Hippo	6.5	3.7	11.6	7.5	6.1	9.7	20.4
AD 4 Hippo	13.8	10.7	17.1	18.8	17.6	23.3	5.6
AD 5 Hippo	52.9	53.2	39.2	38.4	42.6	34.6	57.4
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1
Control 2 Hippo	10.6	18.7	17.9	29.5	32.5	29.9	28.5
Control 4 Hippo	51.8	27.0	38.4	32.3	37.9	54.7	86.5
Control (Path) 3 Hippo	9.8	4.6	10.2	6.0	6.4	5.8	0.0
AD 1 Temporal Ctx	10.1	12.9	12.1	17.1	24.5	12.6	16.8
AD 2 Temporal Ctx	33.7	31.0	36.6	39.8	27.5	59.0	21.6
AD 3 Temporal Ctx	0.0	6.0	11.7	11.3	9.0	17.1	5.7
AD 4 Temporal Ctx	12.8	20.2	15.6	25.3	30.4	29.9	8.7
AD 5 Inf Temporal Ctx	59.0	39.2	43.8	36.3	41.8	41.8	73.7

AD 5 Sup Temporal Ctx	21.9	42.0	56.6	32.3	38.7	39.2	55.9
AD 6 Inf Temporal Ctx	73.7	49.3	40.9	46.7	47.6	48.6	76.8
AD 6 Sup Temporal Ctx	50.3	48.3	44.1	50.3	50.3	17.0	59.9
Control 1 Temporal Ctx	11.9	12.9	11.9	15.6	24.0	23.3	46.7
Control 2 Temporal Ctx	18.6	18.2	16.7	17.4	14.9	43.5	50.0
Control 3 Temporal Ctx	6.0	9.6	13.0	14.5	16.5	9.2	9.5
Control 3 Temporal Ctx	25.7	15.2	18.9	13.1	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	18.0	27.0	32.5	30.6	39.8	51.1	46.0
Control (Path) 2 Temporal Ctx	18.4	16.0	19.5	20.4	24.8	7.2	0.0
Control (Path) 3 Temporal Ctx	5.6	7.5	12.9	10.9	11.9	9.9	31.0
Control (Path) 4 Temporal Ctx	16.8	17.1	19.8	18.2	21.6	14.9	39.5
AD 1 Occipital Ctx	11.9	10.2	16.2	11.5	16.0	5.8	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	8.3	6.4	11.7	8.8	10.2	7.8	4.9

AD 4 Occipital Ctx	5.8	13.0	12.6	17.9	18.6	35.4	11.1
AD 5 Occipital Ctx	25.2	25.3	16.7	22.5	22.7	16.6	42.3
AD 6 Occipital Ctx	19.8	20.2	17.8	17.0	22.1	23.5	14.8
Control 1 Occipital Ctx	6.6	6.0	11.3	8.7	7.2	15.2	8.8
Control 2 Occipital Ctx	15.7	26.4	24.8	33.2	29.3	35.8	82.4
Control 3 Occipital Ctx	5.7	10.7	16.4	17.1	19.2	4.4	8.8
Control 4 Occipital Ctx	21.6	12.0	12.1	12.6	13.6	12.9	24.0
Control (Path) 1 Occipital Ctx	28.3	35.6	32.8	36.1	39.5	22.4	100.0
Control (Path) 2 Occipital Ctx	49.7	6.7	9.6	7.9	7.0	5.0	9.3
Control (Path) 3 Occipital Ctx	0.0	5.4	8.4	6.0	5.9	6.7	4.1
Control (Path) 4 Occipital Ctx	6.6	13.2	15.9	10.2	11.4	11.9	32.8
Control 1 Parietal Ctx	8.8	8.8	15.2	16.3	15.7	33.2	9.2
Control 2 Parietal Ctx	14.5	34.4	39.5	28.3	37.1	17.4	28.1
Control 3 Parietal Ctx	19.9	11.5	14.5	8.7	10.8	21.6	9.1
Control (Path) 1 Parietal Ctx	37.6	34.2	33.4	39.2	37.9	47.3	69.3
Control (Path) 2 Parietal Ctx	16.6	19.6	20.0	22.5	18.7	17.1	37.6
Control (Path) 3 Parietal Ctx	0.0	3.9	15.0	7.1	12.0	11.7	10.4

Control (Path) 4 Parietal Ctx	18.2	24.8	28.3	8.8	27.9	29.3	27.5

Table AZL. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9

Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AZM. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	0.0	2.6	20.0	8.2	17.4	13.8	17.3	3.7	18.8
Melanoma* Hs688(A).T	0.0	0.0	2.0	0.5	0.8	0.9	0.4	0.0	0.7
Melanoma* Hs688(B).T	0.0	0.2	4.1	0.6	2.5	2.2	2.9	0.8	2.4
Melanoma* M14	0.0	0.0	0.7	0.7	0.4	0.4	0.4	0.0	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	0.0	2.2	30.4	22.5	18.2	14.6	18.3	3.0	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.0	0.1
Testis Pool	0.0	3.5	8.8	4.2	10.4	9.0	9.1	3.0	9.9
Prostate ca.* (bone met) PC-3	0.0	0.5	2.5	1.0	1.9	1.8	1.3	1.2	4.3
Prostate Pool	0.0	1.0	11.5	8.5	11.3	12.1	28.5	2.1	10.0
Placenta	0.0	0.0	0.7	0.1	0.1	0.1	0.5	0.0	0.4
Uterus Pool	0.0	1.5	4.5	2.6	4.6	4.5	5.3	2.3	4.1
Ovarian ca. OVCAR-3	0.0	0.3	1.1	0.8	0.7	1.1	1.6	0.4	4.0
Ovarian ca. SK-OV-3	0.0	0.2	1.7	1.5	0.8	0.9	1.3	0.5	1.7
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.5	0.4	0.8	0.9	0.0	0.5
Ovarian ca. OVCAR-5	0.0	1.3	2.9	1.5	1.3	1.7	1.4	4.2	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	77.9	90.8	84.7	97.9	69.3	**100.0**	75.8

Ovarian ca. OVCAR-8	5.6	21.9	14.0	11.9	15.6	14.6	17.3	18.2	16.7
Ovary	0.0	0.3	5.2	2.1	3.1	2.3	2.8	0.8	2.4
Breast ca. MCF-7	0.0	0.0	0.3	0.4	0.1	0.2	0.5	0.3	0.5
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.4	0.2	0.2	0.2	0.0	0.3
Breast ca. BT 549	0.0	0.0	0.5	0.3	0.1	0.5	0.6	0.0	0.4
Breast ca. T47D	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.3	0.5
Breast ca. MDA-N	0.0	0.0	0.7	0.7	0.6	0.6	0.6	0.3	0.8
Breast Pool	0.0	4.1	21.8	19.5	14.6	10.7	12.2	3.5	16.7
Trachea	0.0	0.7	8.4	2.9	4.8	4.2	4.7	1.4	5.6
Lung	0.0	0.7	2.3	1.3	4.2	3.2	3.9	5.3	5.1
Fetal Lung	0.0	0.3	9.1	4.0	5.0	4.8	5.3	2.9	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	2.7	3.3	2.6	4.0	2.0	2.3
Lung ca. LX-1	3.1	2.7	6.5	7.0	5.0	3.5	4.9	6.3	44.1
Lung ca. NCI-H146	0.0	0.0	0.3	0.5	0.1	0.2	0.1	0.0	0.1
Lung ca. SHP-77	2.3	0.4	6.8	6.3	5.3	4.5	4.5	0.8	3.8
Lung ca. A549	0.0	2.6	0.9	0.3	0.0	0.4	0.6	2.2	4.7
Lung ca. NCI-H526	0.0	0.0	0.9	0.7	0.6	0.3	0.4	0.3	0.5
Lung ca. NCI-H23	0.0	1.0	4.6	4.5	4.8	3.2	2.9	2.3	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.0	0.0	0.5	0.6	1.0	0.6	0.5	0.0	0.7
Lung ca. NCI-H522	0.0	0.6	2.3	2.4	1.7	1.3	3.3	2.5	8.9

Liver	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.4	2.0
Fetal Liver	0.0	0.3	1.1	0.6	0.6	0.5	0.8	0.8	8.2
Liver ca. HepG2	0.0	0.3	0.2	0.1	0.0	0.2	0.1	0.9	2.4
Kidney Pool	6.5	0.0	47.0	34.9	33.9	28.1	43.2	14.6	32.8
Fetal Kidney	0.0	0.0	4.9	5.1	4.1	4.0	5.8	3.4	11.5
Renal ca. 786-0	0.0	0.0	0.2	0.2	0.3	0.1	0.3	0.0	0.9
Renal ca. A498	0.0	1.8	0.2	0.1	0.0	0.3	0.5	3.8	8.5
Renal ca. ACHN	0.0	0.5	2.5	0.7	1.7	1.5	1.2	0.5	2.5
Renal ca. UO-31	0.0	0.0	0.5	0.3	0.2	0.2	0.6	0.0	0.3
Renal ca. TK-10	0.0	0.4	3.1	2.5	2.0	1.9	2.1	0.5	4.6
Bladder	0.0	0.0	5.9	3.0	5.5	5.1	8.3	0.9	6.7
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.7	0.9	1.2	1.1	0.8	6.7
Gastric ca. KATO III	0.0	0.5	0.8	0.4	0.2	0.3	0.4	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.0	0.2	0.2	0.3	2.2	1.2
Colon ca. SW480	9.5	5.2	41.8	39.0	27.0	23.3	23.0	6.3	33.7
Colon ca.* (SW480 met) SW620	7.7	4.8	16.4	15.5	12.8	10.3	6.1	7.2	25.0
Colon ca. HT29	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.3	0.3
Colon ca. HCT-116	1.6	0.2	3.2	3.8	2.5	2.0	2.1	0.6	4.3
Colon ca. CaCo-2	10.4	3.6	27.0	22.2	19.1	16.7	18.3	6.5	38.2
Colon cancer tissue	0.0	3.3	11.0	6.5	11.9	7.6	7.7	4.4	20.4
Colon ca. SW1116	0.0	3.0	2.5	1.7	2.0	1.5	1.8	2.1	6.0

Colon ca. Colo-205	0.0	0.4	0.3	0.2	0.2	0.0	0.2	1.3	0.8
Colon ca. SW-48	0.0	3.6	1.4	1.3	1.5	1.5	1.4	3.0	2.6
Colon Pool	0.0	5.0	28.1	28.7	23.2	18.7	25.5	8.1	20.6
Small Intestine Pool	0.0	1.7	17.1	10.5	11.2	13.0	12.8	2.0	10.4
Stomach Pool	0.0	2.3	14.3	6.2	9.5	9.3	8.5	4.2	10.7
Bone Marrow Pool	0.0	1.6	14.3	11.3	10.2	8.7	18.7	3.5	12.5
Fetal Heart	0.0	2.3	25.5	24.3	24.5	21.8	33.7	8.6	20.7
Heart Pool	5.2	7.0	29.7	23.0	25.9	17.2	33.7	10.7	26.1
Lymph Node Pool	0.0	6.1	33.7	30.4	22.1	23.7	19.9	6.7	24.7
Fetal Skeletal Muscle	36.9	5.2	54.3	46.7	48.6	46.3	19.1	19.2	50.7
Skeletal Muscle Pool	12.3	9.2	29.3	21.5	29.5	25.9	22.1	22.7	32.3
Spleen Pool	0.0	0.0	1.9	2.0	2.0	1.7	2.7	0.6	3.1
Thymus Pool	0.0	2.0	10.4	7.5	8.1	9.4	7.7	3.1	7.0
CNS cancer (glio/astro) U87-MG	1.6	1.5	14.9	6.1	10.7	10.0	10.9	2.2	14.1
CNS cancer (glio/astro) U-118-MG	0.0	0.3	4.7	2.9	3.8	3.1	3.8	0.8	5.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	2.6	1.7	2.1	1.0	1.4	0.5	2.6
CNS cancer (astro) SF-539	0.0	0.0	0.0	0.2	0.1	0.2	0.1	0.2	0.1
CNS cancer (astro) SNB-75	1.9	1.1	14.9	5.9	6.5	10.0	11.7	2.8	9.7

CNS cancer (glio) SNB-19	84.1	79.0	100.0	100.0	100.0	100.0	100.0	97.9	100.0
CNS cancer (glio) SF-295	1.8	0.0	11.3	9.0	8.0	7.8	8.2	1.5	14.8
Brain (Amygdala) Pool	2.3	0.8	7.7	6.9	6.2	4.8	8.0	4.4	5.3
Brain (cerebellum)	6.6	0.4	19.8	11.1	10.7	9.7	8.8	1.2	9.7
Brain (fetal)	3.0	0.7	12.7	11.5	6.6	5.6	6.8	2.1	6.4
Brain (Hippocampus) Pool	3.1	3.2	11.7	11.0	8.6	6.9	11.0	4.3	10.2
Cerebral Cortex Pool	1.7	0.6	11.0	7.5	7.5	0.7	11.6	2.0	8.7
Brain (Substantia nigra) Pool	1.8	2.2	11.7	8.5	10.4	4.7	10.0	2.0	9.3
Brain (Thalamus) Pool	0.0	2.7	13.2	10.0	9.3	0.2	9.7	2.8	8.7
Brain (whole)	0.0	0.4	10.6	8.0	5.8	0.3	5.6	1.9	8.7
Spinal Cord Pool	3.2	2.3	14.7	12.8	11.0	7.6	12.2	4.2	9.0
Adrenal Gland	0.0	0.3	9.9	6.1	3.9	3.7	4.8	0.9	4.1
Pituitary gland Pool	0.0	0.0	1.1	0.8	1.2	1.1	1.4	0.6	0.5
Salivary Gland	0.0	0.0	1.8	1.1	1.3	0.9	1.1	0.0	1.0
Thyroid (female)	0.0	0.3	3.1	0.8	2.5	2.5	1.9	1.3	2.3
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.8	0.7	0.6	0.7	0.6	2.2
Pancreas Pool	0.0	0.0	2.0	1.1	1.1	1.6	3.2	1.0	2.3

Table AZN. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6440, Run 268760825
Secondary Th1 act	0.0	1.3	0.0	0.7	0.0	0.0
Secondary Th2 act	0.0	1.2	0.0	0.8	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.0	0.4	0.0	0.0
Primary Tr1 act	0.0	0.7	0.0	0.7	0.0	0.0
Primary Th1 rest	0.0	0.1	0.0	0.3	1.2	0.0
Primary Th2 rest	0.0	0.4	0.0	0.2	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.0	2.4	2.6	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	0.0	0.7	2.3	0.0
CD8 lymphocyte act	0.0	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0	0.3	0.0	0.0
CD4 lymphocyte none	0.0	0.5	0.0	0.4	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	0.0	1.2	0.0
LAK cells rest	2.7	11.8	0.1	3.8	15.2	0.0
LAK cells IL-2	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	0.1	6.3	9.0	52.9
NK Cells IL-2 rest	0.0	3.4	0.0	2.5	1.4	0.0
Two Way MLR 3 day	0.0	2.2	0.0	1.3	1.4	0.0
Two Way MLR 5 day	0.0	0.8	0.0	0.9	0.0	0.0
Two Way MLR 7 day	13.2	1.1	0.0	2.6	3.7	0.0
PBMC rest	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.0	0.6	0.0	0.7	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0	0.2	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	29.1	0.1	8.1	68.8	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0	2.7	1.8	0.0
Dendritic cells none	13.8	4.1	0.0	5.3	0.0	0.0
Dendritic cells LPS	0.0	1.0	0.0	0.7	0.0	0.0
Dendritic cells anti-CD40	3.3	0.5	0.0	0.2	0.0	0.0
Monocytes rest	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	0.0	5.7	0.0	1.8	2.6	0.0
Macrophages rest	0.0	0.6	0.0	0.6	0.0	0.0
Macrophages LPS	0.0	5.4	0.1	6.3	9.2	0.0
HUVEC none	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0	0.0

HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.4	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0	0.3	0.0	0.0
Lung Microvascular EC none	0.0	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0	1.5	0.0	0.0
Astrocytes rest	**100.0**	**100.0**	12.0	**100.0**	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	74.2	97.3	**100.0**	74.7	95.9	95.3
KU-812 (Basophil) rest	0.0	0.0	0.0	0.4	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.8	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	0.0	6.7	8.5	0.0
NCI-H292 none	0.0	1.7	0.0	0.6	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.5	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0	0.5	0.0	0.0
NCI-H292 IL-13	0.0	0.9	0.0	0.9	0.0	0.0
NCI-H292 IFN gamma	0.0	0.5	0.0	0.6	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	0.2	65.5	94.0	54.3
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	0.1	39.8	62.9	52.5
Lung fibroblast IL-4	19.1	27.4	0.1	21.2	34.9	0.0
Lung fibroblast IL-9	23.5	24.0	0.1	26.8	96.6	66.0
Lung fibroblast IL-13	4.5	11.9	0.0	10.4	13.4	0.0
Lung fibroblast IFN gamma	15.7	55.9	0.2	46.3	89.5	47.0
Dermal fibroblast CCD1070 rest	0.0	6.0	0.0	6.3	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.0	0.8	2.3	0.0
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.0	1.3	0.0	0.0
Dermal fibroblast IFN gamma	8.5	30.6	0.1	20.2	26.6	0.0
Dermal fibroblast IL-4	4.1	30.8	0.1	19.8	25.5	0.0
Dermal Fibroblasts rest	8.0	54.3	0.1	46.7	47.3	0.0

Neutrophils TNFa+LPS	0.0	0.9	0.0	0.4	0.0	0.0
Neutrophils rest	0.0	0.0	0.0	0.3	0.0	0.0
Colon	4.0	4.6	0.0	9.5	8.4	0.0
Lung	0.0	2.8	0.0	4.6	2.1	0.0
Thymus	0.0	0.0	0.0	0.4	2.4	0.0
Kidney	4.9	7.8	0.1	9.7	5.2	0.0

Table AZO. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	22.7	Bladder cancer NAT 2	1.4
Colon cancer NAT 1	**100.0**	Bladder cancer NAT 3	4.8
Colon cancer 2	0.0	Bladder cancer NAT 4	66.0
Colon cancer NAT 2	15.1	Prostate adenocarcinoma 1	7.5
Colon cancer 3	2.8	Prostate adenocarcinoma 2	8.0
Colon cancer NAT 3	40.1	Prostate adenocarcinoma 3	9.0
Colon malignant cancer 4	9.5	Prostate adenocarcinoma 4	9.1
Colon normal adjacent tissue 4	0.9	Prostate cancer NAT 5	9.9
Lung cancer 1	6.6	Prostate adenocarcinoma 6	7.7
Lung NAT 1	0.0	Prostate adenocarcinoma 7	17.3
Lung cancer 2	15.9	Prostate adenocarcinoma 8	0.0
Lung NAT 2	0.0	Prostate adenocarcinoma 9	33.9
Squamous cell carcinoma 3	8.3	Prostate cancer NAT 10	4.9
Lung NAT 3	0.0	Kidney cancer 1	16.5
metastatic melanoma 1	49.0	KidneyNAT 1	7.2

Melanoma 2	1.1	Kidney cancer 2	73.7
Melanoma 3	13.8	Kidney NAT 2	19.2
metastatic melanoma 4	24.0	Kidney cancer 3	21.3
metastatic melanoma 5	31.4	Kidney NAT 3	11.4
Bladder cancer 1	2.1	Kidney cancer 4	25.7
Bladder cancer NAT 1	0.0	Kidney NAT 4	14.9
Bladder cancer 2	19.3		

CNS_neurodegeneration_v1.0

Summary: Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/ Ag6440/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6424/Ag6391 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6424/ Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/Ag6440/Ag6964 Nine experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low

levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6391 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/ Ag6440 Seven experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding

normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

BA. CG88634-01: KIAA1219-like protein.

Expression of gene CG88634-01 was assessed using the primer-probe set Ag3649, described in Table BAA. Results of the RTQ-PCR runs are shown in Tables BAB, BAC, BAD and BAE.

Table BAA. Probe Name Ag3649

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgcaagaattgaatcagtatc-3'	22	1055	768
Probe	TET-5'-cctgccttaaacatctgcctcaaata-3'-TAMRA	26	1077	769
Reverse	5'-catccaccagacagctgatt-3'	20	1123	770

Table BAB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3649, Run 211019464	Tissue Name	Rel. Exp.(%) Ag3649, Run 211019464
AD 1 Hippo	12.1	Control (Path) 3 Temporal Ctx	4.5
AD 2 Hippo	28.3	Control (Path) 4 Temporal Ctx	40.9
AD 3 Hippo	6.7	AD 1 Occipital Ctx	12.2
AD 4 Hippo	7.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	**100.0**	AD 3 Occipital Ctx	6.7
AD 6 Hippo	47.6	AD 4 Occipital Ctx	24.7
Control 2 Hippo	25.2	AD 5 Occipital Ctx	20.0
Control 4 Hippo	9.2	AD 6 Occipital Ctx	46.3
Control (Path) 3 Hippo	7.5	Control 1 Occipital Ctx	6.7
AD 1 Temporal Ctx	18.6	Control 2 Occipital Ctx	52.1

AD 2 Temporal Ctx	30.4	Control 3 Occipital Ctx	17.0
AD 3 Temporal Ctx	5.9	Control 4 Occipital Ctx	6.6
AD 4 Temporal Ctx	24.5	Control (Path) 1 Occipital Ctx	73.2
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	10.9
AD 5 SupTemporal Ctx	48.0	Control (Path) 3 Occipital Ctx	3.3
AD 6 Inf Temporal Ctx	51.4	Control (Path) 4 Occipital Ctx	18.4
AD 6 Sup Temporal Ctx	47.6	Control 1 Parietal Ctx	5.3
Control 1 Temporal Ctx	6.9	Control 2 Parietal Ctx	41.5
Control 2 Temporal Ctx	28.1	Control 3 Parietal Ctx	17.3
Control 3 Temporal Ctx	12.9	Control (Path) 1 Parietal Ctx	65.1
Control 4 Temporal Ctx	6.9	Control (Path) 2 Parietal Ctx	24.8
Control (Path) 1 Temporal Ctx	57.0	Control (Path) 3 Parietal Ctx	5.3
Control (Path) 2 Temporal Ctx	36.3	Control (Path) 4 Parietal Ctx	49.0

Table BAC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3649, Run 219798089	Tissue Name	Rel. Exp.(%) Ag3649, Run 219798089
Adipose	14.5	Renal ca. TK-10	46.0
Melanoma* Hs688(A).T	31.9	Bladder	26.4
Melanoma* Hs688(B).T	25.9	Gastric ca. (liver met.) NCI-N87	99.3
Melanoma* M14	31.6	Gastric ca. KATO III	83.5
Melanoma* LOXIMVI	23.8	Colon ca. SW-948	5.9
Melanoma* SK-MEL-5	44.8	Colon ca. SW480	63.7
Squamous cell carcinoma SCC-4	15.6	Colon ca.* (SW480 met) SW620	41.2
Testis Pool	19.9	Colon ca. HT29	20.6

Prostate ca.* (bone met) PC-3	47.6	Colon ca. HCT-116	26.2
Prostate Pool	19.3	Colon ca. CaCo-2	87.1
Placenta	21.5	Colon cancer tissue	30.6
Uterus Pool	12.3	Colon ca. SW1116	7.9
Ovarian ca. OVCAR-3	73.7	Colon ca. Colo-205	7.0
Ovarian ca. SK-OV-3	51.8	Colon ca. SW-48	8.8
Ovarian ca. OVCAR-4	25.2	Colon Pool	28.3
Ovarian ca. OVCAR-5	44.1	Small Intestine Pool	22.2
Ovarian ca. IGROV-1	18.8	Stomach Pool	11.4
Ovarian ca. OVCAR-8	11.0	Bone Marrow Pool	16.0
Ovary	15.5	Fetal Heart	26.8
Breast ca. MCF-7	35.6	Heart Pool	14.0
Breast ca. MDA-MB-231	77.4	Lymph Node Pool	29.7
Breast ca. BT 549	89.5	Fetal Skeletal Muscle	14.2
Breast ca. T47D	85.9	Skeletal Muscle Pool	13.5
Breast ca. MDA-N	25.2	Spleen Pool	17.0
Breast Pool	27.0	Thymus Pool	25.0
Trachea	23.5	CNS cancer (glio/astro) U87-MG	62.0
Lung	5.7	CNS cancer (glio/astro) U-118-MG	76.3
Fetal Lung	51.4	CNS cancer (neuro;met) SK-N-AS	63.7
Lung ca. NCI-N417	5.1	CNS cancer (astro) SF-539	30.8
Lung ca. LX-1	45.4	CNS cancer (astro) SNB-75	**100.0**
Lung ca. NCI-H146	19.1	CNS cancer (glio) SNB-19	18.8
Lung ca. SHP-77	28.5	CNS cancer (glio) SF-295	84.1
Lung ca. A549	19.9	Brain (Amygdala) Pool	10.6
Lung ca. NCI-H526	12.0	Brain (cerebellum)	65.5
Lung ca. NCI-H23	64.6	Brain (fetal)	36.3

Lung ca. NCI-H460	19.2	Brain (Hippocampus) Pool	11.4
Lung ca. HOP-62	8.2	Cerebral Cortex Pool	19.9
Lung ca. NCI-H522	27.5	Brain (Substantia nigra) Pool	10.0
Liver	3.0	Brain (Thalamus) Pool	22.4
Fetal Liver	16.6	Brain (whole)	20.9
Liver ca. HepG2	27.0	Spinal Cord Pool	11.3
Kidney Pool	26.1	Adrenal Gland	25.3
Fetal Kidney	34.2	Pituitary gland Pool	11.2
Renal ca. 786-0	25.5	Salivary Gland	9.5
Renal ca. A498	12.7	Thyroid (female)	6.0
Renal ca. ACHN	21.9	Pancreatic ca. CAPAN2	33.4
Renal ca. UO-31	0.0	Pancreas Pool	28.1

Table BAD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3649, Run 169975759	Tissue Name	Rel. Exp.(%) Ag3649, Run 169975759
Secondary Th1 act	57.4	HUVEC IL-1beta	55.5
Secondary Th2 act	67.8	HUVEC IFN gamma	66.4
Secondary Tr1 act	81.8	HUVEC TNF alpha + IFN gamma	50.0
Secondary Th1 rest	25.5	HUVEC TNF alpha + IL4	40.3
Secondary Th2 rest	47.6	HUVEC IL-11	32.3
Secondary Tr1 rest	41.8	Lung Microvascular EC none	96.6
Primary Th1 act	44.8	Lung Microvascular EC TNFalpha + IL-1beta	97.3
Primary Th2 act	54.3	Microvascular Dermal EC none	55.9
Primary Tr1 act	49.7	Microsvasular Dermal EC TNFalpha + IL-1beta	60.3
Primary Th1 rest	36.3	Bronchial epithelium TNFalpha + IL1beta	47.3
Primary Th2 rest	41.5	Small airway epithelium none	23.7

Primary Tr1 rest	55.1	Small airway epithelium TNFalpha + IL-1beta	45.1
CD45RA CD4 lymphocyte act	38.4	Coronery artery SMC rest	33.7
CD45RO CD4 lymphocyte act	56.3	Coronery artery SMC TNFalpha + IL-1beta	40.1
CD8 lymphocyte act	50.0	Astrocytes rest	40.1
Secondary CD8 lymphocyte rest	51.4	Astrocytes TNFalpha + IL-1beta	29.9
Secondary CD8 lymphocyte act	29.9	KU-812 (Basophil) rest	27.7
CD4 lymphocyte none	42.0	KU-812 (Basophil) PMA/ionomycin	48.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	45.4	CCD1106 (Keratinocytes) none	79.0
LAK cells rest	48.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	**100.0**
LAK cells IL-2	54.7	Liver cirrhosis	17.2
LAK cells IL-2+IL-12	46.3	NCI-H292 none	41.5
LAK cells IL-2+IFN gamma	61.6	NCI-H292 IL-4	71.7
LAK cells IL-2+ IL-18	65.5	NCI-H292 IL-9	**100.0**
LAK cells PMA/ionomycin	46.0	NCI-H292 IL-13	75.3
NK Cells IL-2 rest	65.1	NCI-H292 IFN gamma	72.2
Two Way MLR 3 day	64.6	HPAEC none	43.8
Two Way MLR 5 day	45.1	HPAEC TNF alpha + IL-1 beta	92.0
Two Way MLR 7 day	30.4	Lung fibroblast none	56.3
PBMC rest	29.9	Lung fibroblast TNF alpha + IL-1 beta	27.9
PBMC PWM	31.2	Lung fibroblast IL-4	39.8
PBMC PHA-L	40.3	Lung fibroblast IL-9	53.6
Ramos (B cell) none	47.3	Lung fibroblast IL-13	31.4
Ramos (B cell) ionomycin	49.7	Lung fibroblast IFN gamma	42.9

B lymphocytes PWM	28.5	Dermal fibroblast CCD1070 rest	55.9
B lymphocytes CD40L and IL-4	55.1	Dermal fibroblast CCD1070 TNF alpha	83.5
EOL-1 dbcAMP	46.7	Dermal fibroblast CCD1070 IL-1 beta	36.1
EOL-1 dbcAMP PMA/ionomycin	66.0	Dermal fibroblast IFN gamma	34.9
Dendritic cells none	44.8	Dermal fibroblast IL-4	61.6
Dendritic cells LPS	36.6	Dermal Fibroblasts rest	37.1
Dendritic cells anti-CD40	53.2	Neutrophils TNFa+LPS	14.3
Monocytes rest	58.2	Neutrophils rest	64.6
Monocytes LPS	80.7	Colon	19.9
Macrophages rest	41.2	Lung	30.4
Macrophages LPS	28.7	Thymus	85.3
HUVEC none	28.9	Kidney	45.7
HUVEC starved	52.1		

Table BAE. general oncology screening panel_v_2.4

Tissue Name	**Rel. Exp.(%) Ag3649, Run 267777885**	**Tissue Name**	**Rel. Exp.(%) Ag3649, Run 267777885**
Colon cancer 1	30.4	Bladder cancer NAT 2	2.0
Colon cancer NAT 1	7.7	Bladder cancer NAT 3	4.8
Colon cancer 2	29.7	Bladder cancer NAT 4	14.8
Colon cancer NAT 2	10.7	Prostate adenocarcinoma 1	65.5
Colon cancer 3	76.3	Prostate adenocarcinoma 2	11.0
Colon cancer NAT 3	17.6	Prostate adenocarcinoma 3	36.6
Colon malignant cancer 4	52.9	Prostate adenocarcinoma 4	38.4
Colon normal adjacent tissue 4	20.6	Prostate cancer NAT 5	12.4
Lung cancer 1	20.3	Prostate adenocarcinoma 6	16.4

Lung NAT 1	5.1	Prostate adenocarcinoma 7	20.6
Lung cancer 2	88.9	Prostate adenocarcinoma 8	13.6
Lung NAT 2	9.5	Prostate adenocarcinoma 9	62.9
Squamous cell carcinoma 3	39.8	Prostate cancer NAT 10	10.9
Lung NAT 3	4.4	Kidney cancer 1	39.5
metastatic melanoma 1	31.6	KidneyNAT 1	23.8
Melanoma 2	5.6	Kidney cancer 2	**100.0**
Melanoma 3	4.8	Kidney NAT 2	31.6
metastatic melanoma 4	46.7	Kidney cancer 3	33.9
metastatic melanoma 5	84.7	Kidney NAT 3	8.5
Bladder cancer 1	3.4	Kidney cancer 4	13.5
Bladder cancer NAT 1	0.0	Kidney NAT 4	6.3
Bladder cancer 2	23.7		

CNS_neurodegeneration_v1.0 Summary: Ag3649 This panel does not show differential expression of this gene in Alzheimer's disease. However, this profile confirms the expression of this gene at moderate levels in the brain. See Panel 1.4 for discussion of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3649 Highest expression of this gene is seen in a brain cancer cell line (CT=25). This gene is widely expressed in this panel, with high levels of expression seen in brain, colon, gastric, lung, breast, ovarian, and melanoma cancer cell lines. This expression profile suggests a role for this gene product in cell survival and proliferation. Modulation of this gene product may be useful in the treatment of cancer.

Among tissues with metabolic function, this gene is expressed at high to moderate levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at much higher levels in fetal lung tissue (CT=26) when compared to expression in the adult counterpart (CT=29). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

This gene is also expressed at high to moderate levels in the CNS, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 4.1D Summary: Ag3649 Highest expression of this gene is seen in IL-9 treated NCI-H292 cells and TNF-a and IL-1b treated keratinocytes (CT=27.3). This gene is also expressed at hight to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

general oncology screening panel_v_2.4 Summary: Ag3649 Highest expression of this gene is detected in kidney cancer (CT=27.6). Significant expression of this gene is detected both in normal and cancer samples derived from colon, kidney, bladder, lung, prostate and melanoma. Expression of this gene is higher in cancer samples as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be use as diagnostic marker for lung, colon, prostate, kidney and bladder cancer, as well as metastatic melanoma. In addition, therapeutic modulation of this gene through the use of antibodoy or small molecule drug may be beneficial in the treatment of melenoma, prostate, lung, colon, kidney and bladder cancers.

BB. CG97012-01 and CG97012-02: SEIZURE 6 PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG97012-01 and CG97012-02 was assessed using the primer-probe sets Ag1477 and Ag4105, described in Tables BBA and BBB. Results of the RTQ-PCR runs are shown in Tables BBC, BBD, BBE, BBF, BBG, BBH, BBI and BBJ.

Table BBA. Probe Name Ag1477

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aatcctgaggggtacattgact-3'	22	859	771
Probe	TET-5'-ccctcaacaactttctggagtgcaca-3'-TAMRA	26	902	772
Reverse	5'-agccagtgtagactgtcacgtt-3'	22	931	773

Table BBB. Probe Name Ag4105

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aatcctgaggggtacattgact-3'	22	859	774
Probe	TET-5'-ccctcaacaactttctggagtgcaca-3'-TAMRA	26	902	775
Reverse	5'-agccagtgtagactgtcacgtt-3'	22	931	776

Table BBC. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4105, Run 255325336	Tissue Name	Rel. Exp.(%) Ag4105, Run 255325336
110967 COPD-F	7.7	112427 Match Control Psoriasis-F	1.3
110980 COPD-F	1.9	112418 Psoriasis-M	1.1
110968 COPD-M	0.0	112723 Match Control Psoriasis-M	3.9
110977 COPD-M	4.4	112419 Psoriasis-M	0.0

110989 Emphysema-F	9.6	112424 Match Control Psoriasis-M	1.2
110992 Emphysema-F	1.6	112420 Psoriasis-M	8.2
110993 Emphysema-F	13.8	112425 Match Control Psoriasis-M	5.8
110994 Emphysema-F	0.0	104689 (MF) OA Bone-Backus	6.7
110995 Emphysema-F	0.0	104690 (MF) Adj "Normal" Bone-Backus	1.9
110996 Emphysema-F	0.0	104691 (MF) OA Synovium-Backus	49.3
110997 Asthma-M	4.5	104692 (BA) OA Cartilage-Backus	36.6
111001 Asthma-F	0.0	104694 (BA) OA Bone-Backus	7.9
111002 Asthma-F	1.8	104695 (BA) Adj "Normal" Bone-Backus	3.7
111003 Atopic Asthma-F	5.8	104696 (BA) OA Synovium-Backus	22.1
111004 Atopic Asthma-F	6.9	104700 (SS) OA Bone-Backus	4.2
111005 Atopic Asthma-F	3.1	104701 (SS) Adj "Normal" Bone-Backus	6.6
111006 Atopic Asthma-F	0.0	104702 (SS) OA Synovium-Backus	15.1
111417 Allergy-M	0.0	117093 OA Cartilage Rep7	5.8
112347 Allergy-M	15.2	112672 OA Bone5	3.7
112349 Normal Lung-F	11.0	112673 OA Synovium5	0.0
112357 Normal Lung-F	2.2	112674 OA Synovial Fluid cells5	1.7
112354 Normal Lung-M	7.1	117100 OA Cartilage Rep14	0.0
112374 Crohns-F	25.0	112756 OA Bone9	**100.0**
112389 Match Control Crohns-F	0.9	112757 OA Synovium9	6.0
112375 Crohns-F	8.3	112758 OA Synovial Fluid Cells9	6.3

112732 Match Control Crohns-F	3.3	117125 RA Cartilage Rep2	1.8
112725 Crohns-M	7.4	113492 Bone2 RA	14.8
112387 Match Control Crohns-M	2.7	113493 Synovium2 RA	3.0
112378 Crohns-M	20.9	113494 Syn Fluid Cells RA	11.6
112390 Match Control Crohns-M	6.9	113499 Cartilage4 RA	10.7
112726 Crohns-M	15.3	113500 Bone4 RA	7.1
112731 Match Control Crohns-M	5.9	113501 Synovium4 RA	5.4
112380 Ulcer Col-F	2.1	113502 Syn Fluid Cells4 RA	2.0
112734 Match Control Ulcer Col-F	2.0	113495 Cartilage3 RA	2.0
112384 Ulcer Col-F	2.1	113496 Bone3 RA	14.5
112737 Match Control Ulcer Col-F	1.4	113497 Synovium3 RA	6.8
112386 Ulcer Col-F	4.2	113498 Syn Fluid Cells3 RA	10.5
112738 Match Control Ulcer Col-F	1.9	117106 Normal Cartilage Rep20	0.0
112381 Ulcer Col-M	5.8	113663 Bone3 Normal	8.3
112735 Match Control Ulcer Col-M	39.0	113664 Synovium3 Normal	8.8
112382 Ulcer Col-M	11.1	113665 Syn Fluid Cells3 Normal	8.2
112394 Match Control Ulcer Col-M	2.0	117107 Normal Cartilage Rep22	2.3
112383 Ulcer Col-M	4.9	113667 Bone4 Normal	9.4
112736 Match Control Ulcer Col-M	0.0	113668 Synovium4 Normal	4.7
112423 Psoriasis-F	5.5	113669 Syn Fluid Cells4 Normal	0.0

Table BBD. Ardais Panel v.1.0

Tissue Name	Rel. Exp.(%) Ag1477, Run 263245998	Tissue Name	Rel. Exp.(%) Ag1477, Run 263245998
136799_Lung cancer(362)	5.4	136787_lung cancer(356)	2.4
136800_Lung NAT(363)	49.3	136788_lung NAT(357)	17.8
136813_Lung cancer(372)	5.4	136804_Lung cancer(369)	9.9
136814_Lung NAT(373)	6.2	136805_Lung NAT(36A)	12.8
136815_Lung cancer(374)	18.0	136806_Lung cancer(36B)	1.7
136816_Lung NAT(375)	62.4	136807_Lung NAT(36C)	19.6
136791_Lung cancer(35A)	3.8	136789_lung cancer(358)	15.0
136795_Lung cancer(35E)	1.9	136802_Lung cancer(365)	21.2
136797_Lung cancer(360)	0.0	136803_Lung cancer(368)	7.7
136794_lung NAT(35D)	24.5	136811_Lung cancer(370)	5.1
136818_Lung NAT(377)	33.2	136810_Lung NAT(36F)	**100.0**

Table BBE. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1477, Run 206941434	Rel. Exp.(%) Ag4105, Run 206943848	Tissue Name	Rel. Exp.(%) Ag1477, Run 206941434	Rel. Exp.(%) Ag4105, Run 206943848
AD 1 Hippo	11.9	10.6	Control (Path) 3 Temporal Ctx	2.6	2.6
AD 2 Hippo	33.7	23.3	Control (Path) 4 Temporal Ctx	29.3	17.9
AD 3 Hippo	8.1	7.0	AD 1 Occipital Ctx	7.9	7.7
AD 4 Hippo	5.1	5.0	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	**100.0**	**100.0**	AD 3 Occipital Ctx	3.9	3.2
AD 6 Hippo	49.7	40.9	AD 4 Occipital Ctx	17.2	10.5
Control 2 Hippo	61.1	47.0	AD 5 Occipital Ctx	15.1	55.5
Control 4 Hippo	4.1	3.8	AD 6 Occipital Ctx	69.3	14.1

Control (Path) 3 Hippo	3.7	3.3	Control 1 Occipital Ctx	1.2	0.8
AD 1 Temporal Ctx	6.1	4.7	Control 2 Occipital Ctx	88.3	84.7
AD 2 Temporal Ctx	27.0	23.8	Control 3 Occipital Ctx	16.2	13.4
AD 3 Temporal Ctx	3.1	2.6	Control 4 Occipital Ctx	2.3	2.3
AD 4 Temporal Ctx	14.4	10.3	Control (Path) 1 Occipital Ctx	92.7	73.7
AD 5 Inf Temporal Ctx	66.9	71.2	Control (Path) 2 Occipital Ctx	5.4	7.0
AD 5 SupTemporal Ctx	36.1	32.3	Control (Path) 3 Occipital Ctx	1.1	0.4
AD 6 Inf Temporal Ctx	25.7	25.3	Control (Path) 4 Occipital Ctx	14.1	10.6
AD 6 Sup Temporal Ctx	27.4	22.5	Control 1 Parietal Ctx	3.9	2.2
Control 1 Temporal Ctx	4.5	3.9	Control 2 Parietal Ctx	15.8	19.2
Control 2 Temporal Ctx	52.9	42.0	Control 3 Parietal Ctx	17.4	14.9
Control 3 Temporal Ctx	14.8	11.4	Control (Path) 1 Parietal Ctx	99.3	92.7
Control 4 Temporal Ctx	4.9	4.4	Control (Path) 2 Parietal Ctx	23.7	16.0
Control (Path) 1 Temporal Ctx	69.3	57.8	Control (Path) 3 Parietal Ctx	2.1	2.7
Control (Path) 2 Temporal Ctx	33.0	23.7	Control (Path) 4 Parietal Ctx	58.2	29.5

Table BBF. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag1477, Run 213323518	Rel. Exp.(%) Ag4105, Run 212714156	Tissue Name	Rel. Exp.(%) Ag1477, Run 213323518	Rel. Exp.(%) Ag4105, Run 212714156
Adipose	0.2	0.1	Renal ca. TK-10	0.0	0.0

Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.6	0.3
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW-948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.2	0.1	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT-116	0.0	0.0
Prostate Pool	0.2	0.1	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.0	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	6.5	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.0	0.0	Colon Pool	0.1	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.4	0.2
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	6.0	0.1
Ovarian ca. OVCAR-8	0.0	0.0	Bone Marrow Pool	0.1	0.1
Ovary	0.1	0.1	Fetal Heart	0.1	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.1	0.0
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.3	0.1
Breast ca. BT 549	0.0	0.0	Fetal Skeletal Muscle	0.2	0.0
Breast ca. T47D	0.0	0.1	Skeletal Muscle Pool	0.0	0.0

Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.1	0.1
Breast Pool	0.0	0.1	Thymus Pool	0.2	0.2
Trachea	0.2	0.3	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	1.2	1.0
Fetal Lung	0.6	0.3	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	30.1	11.4	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.3	0.1
Lung ca. NCI-H146	22.2	18.3	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	9.0	4.3	CNS cancer (glio) SF-295	0.0	0.0
Lung ca. A549	0.0	0.0	Brain (Amygdala) Pool	21.8	9.3
Lung ca. NCI-H526	11.0	4.3	Brain (cerebellum)	87.1	54.3
Lung ca. NCI-H23	1.3	0.7	Brain (fetal)	**100.0**	**100.0**
Lung ca. NCI-H460	0.2	0.1	Brain (Hippocampus) Pool	28.9	25.5
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	40.9	15.9
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	29.3	12.1
Liver	0.0	0.0	Brain (Thalamus) Pool	37.9	14.7
Fetal Liver	0.1	0.2	Brain (whole)	43.5	26.4
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	7.5	4.0
Kidney Pool	0.1	0.0	Adrenal Gland	4.3	1.5
Fetal Kidney	0.1	0.0	Pituitary gland Pool	2.9	2.9
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.2	0.1

Renal ca. A498	0.0	0.0	Thyroid (female)	0.1	0.2
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.0	0.0
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.6	0.2

Table BBG. Panel 3D

Tissue Name	Rel. Exp.(%) Ag1477, Run 215538905	Tissue Name	Rel. Exp.(%) Ag1477, Run 215538905
Daoy- Medulloblastoma	0.0	Ca Ski- Cervical epidermoid carcinoma (metastasis)	0.0
TE671- Medulloblastoma	0.0	ES-2- Ovarian clear cell carcinoma	0.0
D283 Med- Medulloblastoma	0.0	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.0	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	0.7	MEG-01- Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78- Glioma	0.0	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	0.0	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	0.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	3.8	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	0.0	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	34.6	JM1- pre-B-cell lymphoma	0.0
Cerebellum	50.7	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	0.3	TF-1- Erythroleukemia	0.0
DMS-114- Small cell lung cancer	0.6	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	**100.0**	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	61.1	KU-812- Myelogenous leukemia	0.0

NCI-H526- Small cell lung cancer	49.0	769-P- Clear cell renal carcinoma	0.0
NCI-N417- Small cell lung cancer	78.5	Caki-2- Clear cell renal carcinoma	0.0
NCI-H82- Small cell lung cancer	23.7	SW 839- Clear cell renal carcinoma	0.0
NCI-H157- Squamous cell lung cancer (metastasis)	0.0	G401- Wilms' tumor	0.0
NCI-H1155- Large cell lung cancer	18.8	Hs766T- Pancreatic carcinoma (LN metastasis)	0.0
NCI-H1299- Large cell lung cancer	0.0	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.0
NCI-H727- Lung carcinoid	1.7	SU86.86- Pancreatic carcinoma (liver metastasis)	0.0
NCI-UMC-11- Lung carcinoid	0.0	BxPC-3- Pancreatic adenocarcinoma	0.0
LX-1- Small cell lung cancer	0.0	HPAC- Pancreatic adenocarcinoma	0.0
Colo-205- Colon cancer	0.0	MIA PaCa-2- Pancreatic carcinoma	0.0
KM12- Colon cancer	0.1	CFPAC-1- Pancreatic ductal adenocarcinoma	0.0
KM20L2- Colon cancer	0.0	PANC-1- Pancreatic epithelioid ductal carcinoma	0.0
NCI-H716- Colon cancer	0.0	T24- Bladder carcinma (transitional cell)	0.0
SW-48- Colon adenocarcinoma	0.0	5637- Bladder carcinoma	0.0
SW1116- Colon adenocarcinoma	0.0	HT-1197- Bladder carcinoma	0.0
LS 174T- Colon adenocarcinoma	0.0	UM-UC-3- Bladder carcinma (transitional cell)	0.0
SW-948- Colon adenocarcinoma	0.0	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	0.0	HT-1080- Fibrosarcoma	0.0
NCI-SNU-5- Gastric carcinoma	0.0	MG-63- Osteosarcoma	0.0

KATO III- Gastric carcinoma	0.0	SK-LMS-1- Leiomyosarcoma (vulva)	0.0
NCI-SNU-16- Gastric carcinoma	0.0	SJRH30- Rhabdomyosarcoma (met to bone marrow)	0.0
NCI-SNU-1- Gastric carcinoma	0.0	A431- Epidermoid carcinoma	0.0
RF-1- Gastric adenocarcinoma	0.2	WM266-4- Melanoma	0.0
RF-48- Gastric adenocarcinoma	0.0	DU 145- Prostate carcinoma (brain metastasis)	0.0
MKN-45- Gastric carcinoma	2.7	MDA-MB-468- Breast adenocarcinoma	0.0
NCI-N87- Gastric carcinoma	0.0	SCC-4- Squamous cell carcinoma of tongue	0.0
OVCAR-5- Ovarian carcinoma	0.0	SCC-9- Squamous cell carcinoma of tongue	0.0
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.0
HelaS3- Cervical adenocarcinoma	0.0	CAL 27- Squamous cell carcinoma of tongue	0.0

Table BBH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag1477, Run 200923970	Rel. Exp.(%) Ag4105, Run 175180105	Tissue Name	Rel. Exp.(%) Ag1477, Run 200923970	Rel. Exp.(%) Ag4105, Run 175180105
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	4.5	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	3.3	0.0	HUVEC IL-11	0.0	0.9
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	7.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0

Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	1.5	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	4.0	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	3.9	Astrocytes rest	4.1	0.0
Secondary CD8 lymphocyte rest	0.0	1.4	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	5.6	2.6	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.6	1.4	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	0.0	2.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	4.1	1.1	Liver cirrhosis	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.0	0.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	11.7	0.0	NCI-H292 IFN gamma	0.0	0.0

Two Way MLR 3 day	4.7	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	0.0	0.0
PBMC rest	26.8	8.5	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	7.2	0.0
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	2.2
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.6
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	0.0
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	3.5	0.0
Dendritic cells none	35.1	11.5	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	9.4	2.3	Dermal Fibroblasts rest	1.6	0.0
Dendritic cells anti-CD40	24.5	14.1	Neutrophils TNFa+LPS	7.5	0.0
Monocytes rest	93.3	37.6	Neutrophils rest	3.8	3.1
Monocytes LPS	5.6	2.5	Colon	17.6	5.8
Macrophages rest	0.0	0.0	Lung	1.2	4.5
Macrophages LPS	1.7	0.0	Thymus	49.3	13.8
HUVEC none	0.0	0.0	Kidney	**100.0**	**100.0**
HUVEC starved	0.0	0.0			

Table BBI. Panel CNS_1.1

Tissue Name	**Rel. Exp.(%) Ag1477, Run 204172546**	**Tissue Name**	**Rel. Exp.(%) Ag1477, Run 204172546**

Cing Gyr Depression2	4.2	BA17 PSP2	3.6
Cing Gyr Depression	2.3	BA17 PSP	11.1
Cing Gyr PSP2	1.3	BA17 Huntington's2	3.4
Cing Gyr PSP	2.9	BA17 Huntington's	13.7
Cing Gyr Huntington's2	4.4	BA17 Parkinson's2	13.5
Cing Gyr Huntington's	27.5	BA17 Parkinson's	7.7
Cing Gyr Parkinson's2	10.4	BA17 Alzheimer's2	1.7
Cing Gyr Parkinson's	9.8	BA17 Control2	21.5
Cing Gyr Alzheimer's2	3.4	BA17 Control	16.6
Cing Gyr Alzheimer's	9.6	BA9 Depression2	3.0
Cing Gyr Control2	19.8	BA9 Depression	2.2
Cing Gyr Control	24.1	BA9 PSP2	2.6
Temp Pole Depression2	2.4	BA9 PSP	5.1
Temp Pole PSP2	2.9	BA9 Huntington's2	2.0
Temp Pole PSP	0.9	BA9 Huntington's	16.0
Temp Pole Huntington's	13.6	BA9 Parkinson's2	33.2
Temp Pole Parkinson's2	9.4	BA9 Parkinson's	10.2
Temp Pole Parkinson's	7.2	BA9 Alzheimer's2	3.6
Temp Pole Alzheimer's2	1.3	BA9 Alzheimer's	1.1
Temp Pole Alzheimer's	2.2	BA9 Control2	**100.0**
Temp Pole Control2	15.8	BA9 Control	8.7
Temp Pole Control	6.2	BA7 Depression	3.6
Glob Palladus Depression	0.8	BA7 PSP2	7.8
Glob Palladus PSP2	1.5	BA7 PSP	19.3
Glob Palladus PSP	0.5	BA7 Huntington's2	7.6
Glob Palladus Parkinson's2	0.8	BA7 Huntington's	13.1

Glob Palladus Parkinson's	13.4	BA7 Parkinson's2	16.8
Glob Palladus Alzheimer's2	1.3	BA7 Parkinson's	2.7
Glob Palladus Alzheimer's	3.1	BA7 Alzheimer's2	1.3
Glob Palladus Control2	1.9	BA7 Control2	14.4
Glob Palladus Control	1.0	BA7 Control	14.5
Sub Nigra Depression2	1.5	BA4 Depression2	3.1
Sub Nigra Depression	0.8	BA4 Depression	6.8
Sub Nigra PSP2	1.2	BA4 PSP2	15.1
Sub Nigra Huntington's2	10.6	BA4 PSP	4.6
Sub Nigra Huntington's	15.1	BA4 Huntington's2	0.9
Sub Nigra Parkinson's2	12.5	BA4 Huntington's	21.6
Sub Nigra Alzheimer's2	2.0	BA4 Parkinson's2	40.3
Sub Nigra Control2	9.0	BA4 Parkinson's	17.1
Sub Nigra Control	8.4	BA4 Alzheimer's2	2.0
BA17 Depression2	6.7	BA4 Control2	26.4
BA17 Depression	2.0	BA4 Control	12.5

Table BBJ. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag1477, Run 259733191	Tissue Name	Rel. Exp.(%) Ag1477, Run 259733191
Colon cancer 1	2.8	Bladder NAT 2	0.0
Colon NAT 1	12.6	Bladder NAT 3	0.0
Colon cancer 2	10.9	Bladder NAT 4	1.4
Colon NAT 2	0.0	Prostate adenocarcinoma 1	**100.0**
Colon cancer 3	0.0	Prostate adenocarcinoma 2	4.9
Colon NAT 3	30.6	Prostate adenocarcinoma 3	17.7

Colon malignant cancer 4	0.0	Prostate adenocarcinoma 4	0.0
Colon NAT 4	1.3	Prostate NAT 5	8.2
Lung cancer 1	5.8	Prostate adenocarcinoma 6	7.0
Lung NAT 1	0.0	Prostate adenocarcinoma 7	2.8
Lung cancer 2	42.0	Prostate adenocarcinoma 8	5.6
Lung NAT 2	0.0	Prostate adenocarcinoma 9	48.6
Squamous cell carcinoma 3	0.0	Prostate NAT 10	0.0
Lung NAT 3	0.0	Kidney cancer 1	0.0
Metastatic melanoma 1	5.3	Kidney NAT 1	6.1
Melanoma 2	2.1	Kidney cancer 2	9.7
Melanoma 3	0.9	Kidney NAT 2	0.0
Metastatic melanoma 4	11.8	Kidney cancer 3	1.8
Metastatic melanoma 5	17.7	Kidney NAT 3	0.0
Bladder cancer 1	1.3	Kidney cancer 4	0.0
Bladder NAT 1	0.0	Kidney NAT 4	0.0
Bladder cancer 2	0.0		

AI_comprehensive panel_v1.0 Summary: Ag4105 Highest expression in an sample from OA bone (CT=31.4). Low to moderate levels of expression of this gene are detected in samples derived from osteoarthritic (OA) bone and adjacent bone as well as OA cartilage and OA synovium. Low level expression is also detected in cartilage, bone, and synovial fluid samples from rheumatoid arthritis patients. Low level expression is also detected in samples derived from normal lung samples, COPD lung, emphysema, allergy, Crohn's disease (normal matched control and diseased), and ulcerative colitis (normal matched control and diseased). Therefore, therapeutic modulation of this gene product may ameliorate symptoms/conditions associated with autoimmune and inflammatory disorders including psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

Ardais Panel v.1.0 Summary: Ag1477 Highest expression of this gene is seen in normal lung tissue adjacent to a tumor (CT=31.6). In addition, this gene is expressed at low but significant levels in both lung tumor and normal tissue. The expression in normal adjacent tissue is however, higher compared to the tumor tissue. Therefore, therapeutic modulation of this gene or its protein product may be useful in the treatment of lung cancer

CNS_neurodegeneration_v1.0 Summary: Ag1477/Ag4105 Two experiments with the same probe and primer set produce results that are in excellent agreement. This panel confirms expression of this gene at high levels in the brain, with highest expression detected in the hippocampus of an Alzheimer's patient (CTs=25-26). In addition, this gene appears to be slightly down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this receptor may be of use in reversing the dementia, memory loss, and neuronal death associated with this disease.

General_screening_panel_v1.4 Summary: Ag1477/Ag4105 Two experiments with the same probe and primer set produce results that are in excellent agreement. Highest expression of this gene is detected in the fetal brain (CT=25-26). In addition, high to moderate levels of expression of this gene are seen in all regions of the CNS examined, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurological disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

In addition, this gene is expressed in a cluster of cell line samples derived from lung cancer. This gene is homologous to seizure-related gene 6, a gene clearly involved in lung tumorogenesis. The genetic data from Nishioka *et al.* point to its genomic region as being involved in lung tumors. While the region itself is often deleted, the expression indicates that the deleted regions might be regulatory region(s) that normally repress the expression of this gene in lung tumor cells. Therefore, targeting this gene with a human monoclonal antibody that results in an inhibition of the activity of this protein, preferably as it relates to its apoptotic/survival activity in tumor cells, specifically lung tumor cells, may have a therapeutic effect on all solid tumor that depend on its activity, preferably on lung tumors.

References:

1. Nishioka M. Oncogene 2000 Dec 14;19(54):6251-60

2. Shimizu-Nishikawa K. Biochem Biophys Res Commun 1995 Nov 2;216(1):382-9

Panel 3D Summary: Ag1477 Expression in this panel is consistent with expression in Panel 1.4, with expression detected in samples derived from cerebellum and lung cancer cell lines only.

Panel 4.1D Summary: Ag1477/Ag4105 Two experiments with the same probe and primer set produce results that are in excellent agreement. Highest expression is seen in the kidney, with moderate to low levels of expression seen in resting monocytes, and dendritic cells. The transcript is more highly expressed in resting monocytes and dendritic cells than in treated cells of these types. Thus, the protein encoded by this transcript may be important in monocytic and dendritic cell differentiation and activation. Therefore, regulating the expression of this transcript or the function of the protein it encodes may alter the types and levels of monocytic cells regulated by cytokine and chemokine production and T cell activation. Therapeutics designed with the protein encoded by this transcript could therefore be important for the treatment of asthma, emphysema, inflammatory bowel disease, arthritis and psoriasis.

Panel 5D Summary: Ag1477 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Panel CNS_1.1 Summary: Ag1477 This panel confirms the expression of this gene at moderate levels in the brain. See Panels 1.4 and CNS_neurodegeneration_v1.0 for discussion of this gene in the central nervous system.

general oncology screening panel_v_2.4 Summary: Ag1477 Highest expression of this gene is seen in prostate cancer (CT=33). Low but significant levels of expression are also seen in a lung cancer and normal colon. Hence the product of this gene can be used as a marker and therapeutic modulation may lead to treatment of cancer.

BC. CG97012-03: SEIZURE 6 PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG97012-03 was assessed using the primer-probe set Ag6660, described in Table BCA. Results of the RTQ-PCR runs are shown in Tables BCB and BCC.

Table BCA. Probe Name Ag6660

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tatgacatcgtggggagtga-3'	20	1159	777
Probe	TET-5'-ctcacctgccagtgggacctcag-3'-TAMRA	23	1183	778
Reverse	5'-gactcctccgttttctcacaa-3'	21	1227	779

Table BCB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6660, Run 276247136	Tissue Name	Rel. Exp.(%) Ag6660, Run 276247136
AD 1 Hippo	14.8	Control (Path) 3 Temporal Ctx	2.0
AD 2 Hippo	31.0	Control (Path) 4 Temporal Ctx	26.4
AD 3 Hippo	0.0	AD 1 Occipital Ctx	3.3
AD 4 Hippo	8.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	63.3	AD 3 Occipital Ctx	2.9
AD 6 Hippo	66.0	AD 4 Occipital Ctx	11.7
Control 2 Hippo	76.3	AD 5 Occipital Ctx	47.6
Control 4 Hippo	3.9	AD 6 Occipital Ctx	11.9
Control (Path) 3 Hippo	2.2	Control 1 Occipital Ctx	0.8
AD 1 Temporal Ctx	2.7	Control 2 Occipital Ctx	71.2
AD 2 Temporal Ctx	20.0	Control 3 Occipital Ctx	8.7
AD 3 Temporal Ctx	2.7	Control 4 Occipital Ctx	0.0
AD 4 Temporal Ctx	11.8	Control (Path) 1 Occipital Ctx	**100.0**
AD 5 Inf Temporal Ctx	83.5	Control (Path) 2 Occipital Ctx	9.3
AD 5 Sup Temporal Ctx	53.6	Control (Path) 3 Occipital Ctx	1.4
AD 6 Inf Temporal Ctx	29.5	Control (Path) 4 Occipital Ctx	10.9
AD 6 Sup Temporal Ctx	31.0	Control 1 Parietal Ctx	1.8

Control 1 Temporal Ctx	0.4	Control 2 Parietal Ctx	22.8
Control 2 Temporal Ctx	47.3	Control 3 Parietal Ctx	13.9
Control 3 Temporal Ctx	8.2	Control (Path) 1 Parietal Ctx	87.1
Control 3 Temporal Ctx	4.4	Control (Path) 2 Parietal Ctx	17.3
Control (Path) 1 Temporal Ctx	80.1	Control (Path) 3 Parietal Ctx	1.4
Control (Path) 2 Temporal Ctx	32.8	Control (Path) 4 Parietal Ctx	48.3

Table BCC. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6660, Run 277258095	Tissue Name	Rel. Exp.(%) Ag6660, Run 277258095
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0

Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	0.0	Thymus Pool	0.1
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	1.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	12.2	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	18.7	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.7	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	31.6
Lung ca. NCI-H526	4.9	Brain (cerebellum)	99.3
Lung ca. NCI-H23	0.0	Brain (fetal)	**100.0**
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	39.2
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	53.6
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	21.0
Liver	0.0	Brain (Thalamus) Pool	73.2
Fetal Liver	0.0	Brain (whole)	67.4
Liver ca. HepG2	0.0	Spinal Cord Pool	3.6
Kidney Pool	0.0	Adrenal Gland	1.0
Fetal Kidney	0.0	Pituitary gland Pool	1.6

Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.2	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag6660 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.6 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6660 Highest expression of this gene is detected in fetal brain and cerebellum (CTs=28.8). In addition, moderate levels of expression of this gene is mainly seen in all the regions of central nervous system including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. This gene codes for a variant of Seizure related gene 6 like (SEZ-6/SEZ6L). The expression pattern of this gene is similar to the the one reported in mouse (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28:201-10, PMID: 7723619 ; Biochem Biophys Res Commun 216(1):382-9, PMID: 7488116). Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Moderate levels of expression of this gene is also seen in three of the lung cancer cell lines. Furthermore, genetic and/or epigenetic SEZ6L alterations are involved in the development and/or progression in a subset of lung cancer (Nishioka *et al.*, 2000, Oncogene 19(54):6251-60, PMID: 11175339). Therefore, therapeutic modulation of this gene product through the use of antibodies or small molecule targe may be useful in the treatment of lung cancer.

Panel 4.1D Summary: Ag6660 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

BD. CG99754-01: RIKEN-like protein

Expression of gene CG99754-01 was assessed using the primer-probe sets Gpcr07 and Ag07Gpcr, described in Tables BDA and BDB. Results of the RTQ-PCR runs are shown in Tables BDC, BDD, BDE, BDF and BDG.

Table BDA. Probe Name Gpcr07

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctggaggttggcgacaatg-3'	19	511	780
Probe	TET-5'-cctcgtctacatctctcaccgcgcc-3'-TAMRA	25	531	781
Reverse	5'-ctgctccaggctgttgagg-3'	19	564	782

Table BDB. Probe Name Ag07Gpcr

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctggaggttggcgacaatg-3'	19	511	783
Probe	TET-5'-cctcgtctacatctctcaccgcgcc-3'-TAMRA	25	531	784
Reverse	5'-ctgctccaggctgttgagg-3'	19	564	785

Table BDC. CNS_neurodegeneration_v1.0.

Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 206989718	Rel. Exp.(%) Gpcr07, Run 224996509	Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 206989718	Rel. Exp.(%) Gpcr07, Run 224996509
AD 1 Hippo	26.2	8.5	Control (Path) 3 Temporal Ctx	2.0	5.6
AD 2 Hippo	64.2	30.4	Control (Path) 4 Temporal Ctx	42.9	41.2
AD 3 Hippo	3.5	9.4	AD 1 Occipital Ctx	14.3	15.6
AD 4 Hippo	11.3	8.2	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	59.9	78.5	AD 3 Occipital Ctx	3.6	5.0
AD 6 Hippo	81.2	40.9	AD 4 Occipital Ctx	23.8	18.8

Control 2 Hippo	53.2	39.5	AD 5 Occipital Ctx	28.5	16.8
Control 4 Hippo	11.2	6.0	AD 6 Occipital Ctx	57.0	57.0
Control (Path) 3 Hippo	3.3	4.5	Control 1 Occipital Ctx	0.0	4.6
AD 1 Temporal Ctx	17.2	11.7	Control 2 Occipital Ctx	46.0	68.8
AD 2 Temporal Ctx	34.2	30.1	Control 3 Occipital Ctx	21.5	18.8
AD 3 Temporal Ctx	1.7	7.7	Control 4 Occipital Ctx	3.4	6.2
AD 4 Temporal Ctx	28.3	18.7	Control (Path) 1 Occipital Ctx	94.0	**100.0**
AD 5 Inf Temporal Ctx	95.3	66.9	Control (Path) 2 Occipital Ctx	19.8	10.9
AD 5 SupTemporal Ctx	53.6	47.3	Control (Path) 3 Occipital Ctx	1.3	3.8
AD 6 Inf Temporal Ctx	55.9	36.6	Control (Path) 4 Occipital Ctx	28.9	19.1
AD 6 Sup Temporal Ctx	78.5	37.6	Control 1 Parietal Ctx	7.5	6.6
Control 1 Temporal Ctx	5.3	7.2	Control 2 Parietal Ctx	42.3	42.3
Control 2 Temporal Ctx	61.1	56.3	Control 3 Parietal Ctx	19.1	14.0
Control 3 Temporal Ctx	28.1	18.6	Control (Path) 1 Parietal Ctx	80.7	97.9
Control 4 Temporal Ctx	15.1	9.6	Control (Path) 2 Parietal Ctx	30.6	27.4
Control (Path) 1 Temporal Ctx	**100.0**	85.9	Control (Path) 3 Parietal Ctx	2.0	4.0
Control (Path) 2 Temporal Ctx	57.4	43.2	Control (Path) 4 Parietal Ctx	48.3	46.7

Table BDD. Panel 1

Tissue Name	Rel. Exp.(%) Gpcr07, Run 109664812	Tissue Name	Rel. Exp.(%) Gpcr07, Run 109664812

Endothelial cells	0.0	Renal ca. 786-0	0.0
Endothelial cells (treated)	0.0	Renal ca. A498	0.3
Pancreas	1.3	Renal ca. RXF 393	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. ACHN	0.0
Adrenal gland	1.7	Renal ca. UO-31	0.0
Thyroid	1.3	Renal ca. TK-10	0.0
Salivary gland	3.0	Liver	2.1
Pituitary gland	2.5	Liver (fetal)	3.8
Brain (fetal)	52.5	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	46.3	Lung	0.0
Brain (amygdala)	83.5	Lung (fetal)	0.7
Brain (cerebellum)	19.1	Lung ca. (small cell) LX-1	0.0
Brain (hippocampus)	**100.0**	Lung ca. (small cell) NCI-H69	3.7
Brain (substantia nigra)	43.5	Lung ca. (s.cell var.) SHP-77	0.2
Brain (thalamus)	59.5	Lung ca. (large cell)NCI-H460	2.1
Brain (hypothalamus)	0.7	Lung ca. (non-sm. cell) A549	4.2
Spinal cord	7.5	Lung ca. (non-s.cell) NCI-H23	6.8
glio/astro U87-MG	0.0	Lung ca. (non-s.cell) HOP-62	0.1
glio/astro U-118-MG	0.0	Lung ca. (non-s.cl) NCI-H522	3.8
astrocytoma SW1783	0.0	Lung ca. (squam.) SW 900	0.3
neuro*; met SK-N-AS	0.1	Lung ca. (squam.) NCI-H596	1.6
astrocytoma SF-539	0.8	Mammary gland	6.4
astrocytoma SNB-75	0.0	Breast ca.* (pl.ef) MCF-7	1.3
glioma SNB-19	1.5	Breast ca.* (pl.ef) MDA-MB-231	0.0
glioma U251	0.2	Breast ca.* (pl. ef) T47D	2.6

glioma SF-295	0.0	Breast ca. BT-549	0.0
Heart	5.3	Breast ca. MDA-N	1.3
Skeletal muscle	2.0	Ovary	5.6
Bone marrow	0.7	Ovarian ca. OVCAR-3	6.2
Thymus	0.5	Ovarian ca. OVCAR-4	0.3
Spleen	3.4	Ovarian ca. OVCAR-5	1.1
Lymph node	0.6	Ovarian ca. OVCAR-8	8.0
Colon (ascending)	1.6	Ovarian ca. IGROV-1	2.1
Stomach	1.3	Ovarian ca. (ascites) SK-OV-3	0.1
Small intestine	2.2	Uterus	2.2
Colon ca. SW480	0.5	Placenta	2.8
Colon ca.* SW620 (SW480 met)	0.1	Prostate	1.5
Colon ca. HT29	0.3	Prostate ca.* (bone met) PC-3	0.0
Colon ca. HCT-116	11.3	Testis	6.3
Colon ca. CaCo-2	0.7	Melanoma Hs688(A).T	0.0
Colon ca. HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.1
Colon ca. HCC-2998	0.4	Melanoma UACC-62	9.8
Gastric ca. * (liver met) NCI-N87	0.4	Melanoma M14	3.3
Bladder	2.7	Melanoma LOX IMVI	0.0
Trachea	1.5	Melanoma* (met) SK-MEL-5	4.2
Kidney	2.9	Melanoma SK-MEL-28	2.9
Kidney (fetal)	51.8		

Table BDE. Panel 1.2

Tissue Name	Rel. Exp.(%) Gpcr07, Run 124273559	Rel. Exp.(%) Gpcr07, Run 126539429	Tissue Name	Rel. Exp.(%) Gpcr07, Run 124273559	Rel. Exp.(%) Gpcr07, Run 126539429
Endothelial cells	0.0	0.1	Renal ca. 786-0	0.0	0.0

Heart (Fetal)	2.8	2.8	Renal ca. A498	0.0	0.1
Pancreas	0.3	0.9	Renal ca. RXF 393	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. ACHN	0.0	0.0
Adrenal Gland	1.7	1.5	Renal ca. UO-31	0.0	0.0
Thyroid	0.2	0.7	Renal ca. TK-10	0.0	0.0
Salivary gland	1.3	1.0	Liver	0.7	0.6
Pituitary gland	0.4	0.6	Liver (fetal)	1.3	1.0
Brain (fetal)	17.2	28.1	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (whole)	34.9	39.2	Lung	0.1	0.1
Brain (amygdala)	40.6	29.7	Lung (fetal)	0.6	0.8
Brain (cerebellum)	5.3	9.9	Lung ca. (small cell) LX-1	0.0	0.1
Brain (hippocampus)	45.7	51.1	Lung ca. (small cell) NCI-H69	0.7	0.5
Brain (thalamus)	10.4	15.8	Lung ca. (s.cell var.) SHP-77	0.1	0.1
Cerebral Cortex	**100.0**	**100.0**	Lung ca. (large cell)NCI-H460	0.8	0.5
Spinal cord	3.8	3.1	Lung ca. (non-sm. cell) A549	2.0	1.0
glio/astro U87-MG	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	1.7	0.9
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cell) HOP-62	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	1.4	1.5
neuro*; met SK-N-AS	0.0	0.0	Lung ca. (squam.) SW 900	0.1	0.1
astrocytoma SF-539	0.2	0.2	Lung ca. (squam.) NCI-H596	0.4	0.5
astrocytoma SNB-75	0.0	0.0	Mammary gland	0.8	1.3
glioma SNB-19	0.4	0.3	Breast ca.* (pl.ef) MCF-7	0.2	0.2
glioma U251	0.0	0.1	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0

glioma SF-295	0.0	0.0	Breast ca.* (pl. ef) T47D	0.3	0.6
Heart	2.8	1.6	Breast ca. BT-549	0.0	0.0
Skeletal Muscle	0.6	0.6	Breast ca. MDA-N	0.3	0.2
Bone marrow	0.1	0.1	Ovary	2.5	1.6
Thymus	0.1	0.1	Ovarian ca. OVCAR-3	0.9	1.1
Spleen	0.5	0.6	Ovarian ca. OVCAR-4	0.2	0.1
Lymph node	0.4	0.3	Ovarian ca. OVCAR-5	0.4	0.4
Colorectal Tissue	0.4	0.3	Ovarian ca. OVCAR-8	0.6	0.7
Stomach	0.9	0.8	Ovarian ca. IGROV-1	0.4	0.5
Small intestine	1.7	1.5	Ovarian ca. (ascites) SK-OV-3	0.0	0.1
Colon ca. SW480	0.1	0.1	Uterus	1.1	1.1
Colon ca.* SW620 (SW480 met)	0.1	0.1	Placenta	1.2	1.1
Colon ca. HT29	0.0	0.0	Prostate	0.7	0.4
Colon ca. HCT-116	2.7	2.6	Prostate ca.* (bone met) PC-3	0.0	0.0
Colon ca. CaCo-2	0.2	0.2	Testis	1.4	1.7
Colon ca. Tissue (ODO3866)	0.4	0.3	Melanoma Hs688(A).T	0.0	0.0
Colon ca. HCC-2998	0.1	0.1	Melanoma* (met) Hs688(B).T	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.2	0.2	Melanoma UACC-62	3.0	3.3
Bladder	0.9	1.0	Melanoma M14	0.4	0.7
Trachea	0.5	0.4	Melanoma LOX IMVI	0.0	0.0
Kidney	0.9	1.4	Melanoma* (met) SK-MEL-5	1.0	0.9
Kidney (fetal)	3.9	3.6			

Table BDF. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 181981925	Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 181981925
Secondary Th1 act	0.0	HUVEC IL-1beta	4.6
Secondary Th2 act	0.0	HUVEC IFN gamma	3.1
Secondary Tr1 act	1.1	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	2.1
Secondary Th2 rest	0.0	HUVEC IL-11	1.9
Secondary Tr1 rest	0.0	Lung Microvascular EC none	31.9
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	7.1
Primary Th2 act	0.0	Microvascular Dermal EC none	57.0
Primary Tr1 act	2.0	Microsvasular Dermal EC TNFalpha + IL-1beta	34.2
Primary Th1 rest	1.5	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	1.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	1.7
CD45RA CD4 lymphocyte act	1.1	Coronery artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.9
CD8 lymphocyte act	0.0	Astrocytes rest	1.2
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	6.4
Secondary CD8 lymphocyte act	1.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	2.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.7
LAK cells rest	6.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.9
LAK cells IL-2	0.0	Liver cirrhosis	9.4

LAK cells IL-2+IL-12	0.0	NCI-H292 none	1.1
LAK cells IL-2+IFN gamma	0.1	NCI-H292 IL-4	0.9
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.9
LAK cells PMA/ionomycin	1.1	NCI-H292 IL-13	1.9
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.9
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	2.4	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	1.7
PBMC PWM	0.0	Lung fibroblast IL-4	1.1
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	2.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.2	Dermal fibroblast CCD1070 rest	4.8
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	1.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	1.7	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	35.6	Dermal fibroblast IL-4	1.8
Dendritic cells LPS	30.6	Dermal Fibroblasts rest	1.8
Dendritic cells anti-CD40	31.0	Neutrophils TNFa+LPS	2.2
Monocytes rest	0.0	Neutrophils rest	0.7
Monocytes LPS	4.2	Colon	8.5
Macrophages rest	28.3	Lung	**100.0**
Macrophages LPS	1.3	Thymus	11.2
HUVEC none	0.0	Kidney	77.4
HUVEC starved	3.3		

Table BDG. Panel CNS_1

Tissue Name	Rel. Exp.(%) Gpcr07, Run 182328460	Tissue Name	Rel. Exp.(%) Gpcr07, Run 182328460
BA4 Control	30.8	BA17 PSP	35.8
BA4 Control2	70.2	BA17 PSP2	11.2
BA4 Alzheimer's2	7.1	Sub Nigra Control	11.3
BA4 Parkinson's	23.8	Sub Nigra Control2	2.4
BA4 Parkinson's2	49.7	Sub Nigra Alzheimer's2	5.2
BA4 Huntington's	21.3	Sub Nigra Parkinson's2	11.7
BA4 Huntington's2	17.0	Sub Nigra Huntington's	16.5
BA4 PSP	10.1	Sub Nigra Huntington's2	6.2
BA4 PSP2	38.4	Sub Nigra PSP2	2.8
BA4 Depression	34.2	Sub Nigra Depression	4.0
BA4 Depression2	10.4	Sub Nigra Depression2	3.8
BA7 Control	33.0	Glob Palladus Control	3.0
BA7 Control2	30.4	Glob Palladus Control2	6.3
BA7 Alzheimer's2	9.0	Glob Palladus Alzheimer's	5.2
BA7 Parkinson's	11.7	Glob Palladus Alzheimer's2	4.6
BA7 Parkinson's2	17.2	Glob Palladus Parkinson's	32.8
BA7 Huntington's	36.3	Glob Palladus Parkinson's2	4.3
BA7 Huntington's2	21.8	Glob Palladus PSP	2.4
BA7 PSP	35.8	Glob Palladus PSP2	5.7
BA7 PSP2	23.7	Glob Palladus Depression	3.7
BA7 Depression	10.4	Temp Pole Control	21.6
BA9 Control	29.3	Temp Pole Control2	81.2
BA9 Control2	100.0	Temp Pole Alzheimer's	6.4

BA9 Alzheimer's	7.1	Temp Pole Alzheimer's2	16.0
BA9 Alzheimer's2	20.3	Temp Pole Parkinson's	29.5
BA9 Parkinson's	36.6	Temp Pole Parkinson's2	27.0
BA9 Parkinson's2	39.8	Temp Pole Huntington's	33.0
BA9 Huntington's	40.1	Temp Pole PSP	7.1
BA9 Huntington's2	17.3	Temp Pole PSP2	10.4
BA9 PSP	19.9	Temp Pole Depression2	12.1
BA9 PSP2	8.4	Cing Gyr Control	49.0
BA9 Depression	15.9	Cing Gyr Control2	76.3
BA9 Depression2	12.9	Cing Gyr Alzheimer's	16.8
BA17 Control	40.1	Cing Gyr Alzheimer's2	17.1
BA17 Control2	77.4	Cing Gyr Parkinson's	23.5
BA17 Alzheimer's2	11.9	Cing Gyr Parkinson's2	17.7
BA17 Parkinson's	29.3	Cing Gyr Huntington's	40.6
BA17 Parkinson's2	26.4	Cing Gyr Huntington's2	12.2
BA17 Huntington's	21.8	Cing Gyr PSP	11.8
BA17 Huntington's2	18.8	Cing Gyr PSP2	6.3
BA17 Depression	15.5	Cing Gyr Depression	12.5
BA17 Depression2	28.5	Cing Gyr Depression2	15.2

CNS_neurodegeneration_v1.0 Summary: Ag07Gpcr/ Gpcr07 Two runs with the same probe and primer set produce results that are in excellent agreement. This profile confirms the expression of this gene at moderate levels in the brain. This gene appears to be slightly down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this receptor may be of use in reversing the dementia, memory loss, and neuronal death associated with this disease.

Panel 1 Summary: Gpcr07 Highest expression of this gene is seen in the hippocampus (CT=23), with high levels of detection seen in all regions of the CNS

examined. This gene encodes a leucine-rich repeat protein. Leucine rich repeats (LRR) mediate reversible protein-protein interactions and have diverse cellular functions, including cellular adhesion and signaling. Several of these proteins, such as connectin, slit, chaoptin, and Toll have pivotal roles in neuronal development in Drosophila and may play significant but distinct roles in neural development and in the adult nervous system of humans (Ref. 1). In Drosophilia, the LRR region of axon guidance proteins has been shown to be critical for their function (especially in axon repulsion). Since the leucine-rich-repeat protein encoded by this gene shows high expression in the cerebral cortex, it is an excellent candidate neuronal guidance protein for axons, dendrites and/or growth cones in general. Therefore, therapeutic modulation of the levels of this protein, or possible signaling via this protein, may be of utility in enhancing/directing compensatory synaptogenesis and fiber growth in the CNS in response to neuronal death (stroke, head trauma), axon lesion (spinal cord injury), or neurodegeneration (Alzheimer's, Parkinson's, Huntington's, vascular dementia or any neurodegenerative disease).

Moderate to high levels of expression are also seen in cell lines derived from kidney, breast, colon, melanoma, ovarian cancer, lung cancer, and brain cancer. Therefore, therapeutic modulation of the expression or function of this gene product may be effective in the treatment of these cancers.

Among metabolically relevant tissues, this gene expression is seen in skeletal muscle, thyroid, pancreas, adrenal, heart, adult and fetal liver, and pituitary gland. This observation suggests that therapeutic modulation may aid the treatment of metabolic diseases such as obesity and diabetes as well as neuroendocrine disorders. Glycoprotein hormones influence the development and function of the ovary, testis and thyroid by binding to specific high-affinity receptors. The extracellular domains of these receptors are members of the leucine-rich repeat (LRR) protein superfamily and are responsible for the high-affinity binding.

In addition, this gene is expressed at much higher levels in fetal kidney tissue (CT=24) when compared to expression in the adult counterpart (CT=28). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

References:

1. Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H., Hendrickson W.A., el Tayar N. (1995) Structure 3: 1341-1353.

2. Battye R., Stevens A., Perry R.L., Jacobs J.R. (2001) J. Neurosci. 21: 4290-4298.

3. Itoh A., Miyabayashi T., Ohno M., Sakano S. 1998 Brain Res. Mol. Brain Res. 62: 175-186.

Panel 1.2 Summary: Ag07Gpcr /Gpcr07 Two runs with the same probe and primer set produce results that are in excellent agreement. Highest expression of this gene is seen in the cerebral cortex (CTs=21-22). High levels of expression are seen throughout the CNS, consistent with Panel 1.

Panel 4.1D Summary: Ag07Gpcr Highest expression of this gene is seen in the lung (CT=29.5). Moderate expression is also seen in the kidney, treated and untreated lung and microvascular dermal endothelial cells, treated and untreated dendritic cells, and macrophages. Therefore, therapeutic modulation of this gene may be used for the treatment of autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Panel CNS_1 Summary: Gpcr07 This panel confirms the expression of this gene at high levels in the brain. See Panels 1 and CNS_neurodegeneration_v1.0 for discussion of this gene in the central nervous system.

BE. CG99777-02: CD30 LIGAND-LIKE PROTEIN.

Expression of gene CG99777-02 was assessed using the primer-probe sets Ag6623, Ag6747 and Ag6919, described in Tables BEA, BEB and BEC. Results of the RTQ-PCR runs are shown in Tables BED, BEE and BEF. Note that CG99777-02 represents a full-length physical clone.

Table BEA. Probe Name Ag6623

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agaaagcgcctctctaccatac-3'	22	745	786
Probe	TET-5'-tatttcatccctccaaacacttgggc-3'-TAMRA	26	769	787

Reverse	5'-gaggagaatccttcttggtctaaa-3'	24	806	788

Table BEB. Probe Name Ag6747

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaaggagtggcaaagcatct-3'	20	320	789
Probe	TET-5'-catggagaatgccatctttgttccaa-3'-TAMRA	26	358	790
Reverse	5'-ccagattcccatcctgatatc-3'	21	390	791

Table BEC. Probe Name Ag6919

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctcaaaggagtggcaaagc-3'	20	316	792
Probe	TET-5'-caaaaccaagttgtcttggaacaaagatggcattctcc-3'-TAMRA	38	343	793
Reverse	5'-ccagattcccatcctgatatctga-3'	24	387	794

Table BED. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag6919, Run 308380234	Tissue Name	Rel. Exp.(%) Ag6919, Run 308380234
110967 COPD-F	6.9	112427 Match Control Psoriasis-F	10.0
110980 COPD-F	9.0	112418 Psoriasis-M	3.5
110968 COPD-M	7.0	112723 Match Control Psoriasis-M	2.7
110977 COPD-M	13.0	112419 Psoriasis-M	8.8
110989 Emphysema-F	7.8	112424 Match Control Psoriasis-M	3.3
110992 Emphysema-F	4.5	112420 Psoriasis-M	17.9
110993 Emphysema-F	3.4	112425 Match Control Psoriasis-M	9.6
110994 Emphysema-F	2.6	104689 (MF) OA Bone-Backus	50.3

110995 Emphysema-F	7.1	104690 (MF) Adj "Normal" Bone-Backus	27.9
110996 Emphysema-F	1.3	104691 (MF) OA Synovium-Backus	47.3
110997 Asthma-M	3.3	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	11.3	104694 (BA) OA Bone-Backus	32.8
111002 Asthma-F	9.9	104695 (BA) Adj "Normal" Bone-Backus	27.2
111003 Atopic Asthma-F	8.8	104696 (BA) OA Synovium-Backus	82.4
111004 Atopic Asthma-F	8.0	104700 (SS) OA Bone-Backus	30.6
111005 Atopic Asthma-F	3.8	104701 (SS) Adj "Normal" Bone-Backus	40.9
111006 Atopic Asthma-F	0.8	104702 (SS) OA Synovium-Backus	66.4
111417 Allergy-M	4.4	117093 OA Cartilage Rep7	6.3
112347 Allergy-M	0.0	112672 OA Bone5	11.0
112349 Normal Lung-F	0.0	112673 OA Synovium5	5.8
112357 Normal Lung-F	6.7	112674 OA Synovial Fluid cells5	5.1
112354 Normal Lung-M	3.5	117100 OA Cartilage Rep14	2.8
112374 Crohns-F	4.7	112756 OA Bone9	3.2
112389 Match Control Crohns-F	8.2	112757 OA Synovium9	2.3
112375 Crohns-F	3.3	112758 OA Synovial Fluid Cells9	6.8
112732 Match Control Crohns-F	50.0	117125 RA Cartilage Rep2	7.1
112725 Crohns-M	1.9	113492 Bone2 RA	16.5
112387 Match Control Crohns-M	3.7	113493 Synovium2 RA	5.3
112378 Crohns-M	0.2	113494 Syn Fluid Cells RA	6.0

112390 Match Control Crohns-M	6.7	113499 Cartilage4 RA	9.9
112726 Crohns-M	12.6	113500 Bone4 RA	5.5
112731 Match Control Crohns-M	5.1	113501 Synovium4 RA	5.8
112380 Ulcer Col-F	2.3	113502 Syn Fluid Cells4 RA	6.2
112734 Match Control Ulcer Col-F	**100.0**	113495 Cartilage3 RA	7.8
112384 Ulcer Col-F	6.8	113496 Bone3 RA	9.5
112737 Match Control Ulcer Col-F	4.0	113497 Synovium3 RA	7.5
112386 Ulcer Col-F	4.0	113498 Syn Fluid Cells3 RA	11.3
112738 Match Control Ulcer Col-F	9.2	117106 Normal Cartilage Rep20	0.8
112381 Ulcer Col-M	0.2	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	0.8	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	7.3	113665 Syn Fluid Cells3 Normal	0.1
112394 Match Control Ulcer Col-M	1.4	117107 Normal Cartilage Rep22	1.3
112383 Ulcer Col-M	4.8	113667 Bone4 Normal	1.8
112736 Match Control Ulcer Col-M	3.9	113668 Synovium4 Normal	3.0
112423 Psoriasis-F	5.0	113669 Syn Fluid Cells4 Normal	4.7

Table BEE. General_screening_panel_v1.6

Tissue Name	**Rel. Exp.(%) Ag6919, Run 278388682**	**Tissue Name**	**Rel. Exp.(%) Ag6919, Run 278388682**
Adipose	23.7	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	16.4
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.8
Melanoma* M14	0.0	Gastric ca. KATO III	0.0

Melanoma* LOXIMVI	1.4	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	2.6	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	5.2	Colon ca. CaCo-2	2.4
Placenta	5.7	Colon cancer tissue	15.5
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	15.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	4.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	5.6
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	2.6
Ovary	9.9	Fetal Heart	1.4
Breast ca. MCF-7	0.0	Heart Pool	2.8
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	8.7
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	1.7
Breast ca. MDA-N	0.0	Spleen Pool	11.5
Breast Pool	7.3	Thymus Pool	46.3
Trachea	12.7	CNS cancer (glio/astro) U87-MG	2.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	15.5	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0

Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	4.7	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	2.4
Lung ca. NCI-H526	**100.0**	Brain (cerebellum)	1.8
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	1.7
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	1.0
Fetal Liver	5.6	Brain (whole)	1.7
Liver ca. HepG2	0.0	Spinal Cord Pool	4.3
Kidney Pool	13.9	Adrenal Gland	5.2
Fetal Kidney	3.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	1.8
Renal ca. A498	0.0	Thyroid (female)	0.8
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	1.7

Table BEF. Panel 4.1D

Tissue Name	**Rel. Exp.(%) Ag6747, Run 277641366**	**Rel. Exp.(%) Ag6919, Run 306067437**	**Tissue Name**	**Rel. Exp.(%) Ag6747, Run 277641366**	**Rel. Exp.(%) Ag6919, Run 306067437**
Secondary Th1 act	8.1	8.1	HUVEC IL-1beta	0.1	0.0
Secondary Th2 act	12.3	17.6	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	3.3	5.1	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	3.8	3.4	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	4.0	3.9	HUVEC IL-11	1.4	0.0

Secondary Tr1 rest	6.0	7.1	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	47.3	9.7	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	**100.0**	59.5	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	82.4	**100.0**	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	1.3	1.2	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	1.6	1.7	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.5	0.5	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	6.0	6.8	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	12.4	19.1	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	1.3	1.1	Astrocytes rest	0.0	0.0
Secondary CD8 lymphocyte rest	1.9	1.2	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	1.0	0.4	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	3.1	2.4	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.3	3.0	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	3.6	3.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	1.2	1.2	Liver cirrhosis	0.2	0.3
LAK cells IL-2+IL-12	0.3	0.3	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	1.8	2.1	NCI-H292 IL-4	0.0	0.0

LAK cells IL-2+ IL-18	0.8	0.9	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	12.9	18.7	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	6.4	5.4	NCI-H292 IFN gamma	0.0	0.0
Two Way MLR 3 day	2.1	1.6	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.4	0.6	HPAEC TNF alpha + IL-1 beta	0.2	0.0
Two Way MLR 7 day	0.6	0.5	Lung fibroblast none	0.0	0.0
PBMC rest	1.1	2.1	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.7	0.3	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	1.0	1.2	Lung fibroblast IL-9	0.0	0.0
Ramos (B cell) none	3.6	4.7	Lung fibroblast IL-13	0.0	0.0
Ramos (B cell) ionomycin	15.4	15.1	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	2.6	3.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	4.8	4.1	Dermal fibroblast CCD1070 TNF alpha	6.3	4.6
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.1	0.0	Dermal fibroblast IFN gamma	0.0	0.0
Dendritic cells none	1.6	2.7	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	1.3	1.2	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti-CD40	1.1	1.4	Neutrophils TNFa+LPS	3.7	4.9
Monocytes rest	2.2	3.3	Neutrophils rest	2.1	3.3
Monocytes LPS	9.4	9.4	Colon	0.1	0.0
Macrophages rest	1.1	0.3	Lung	0.1	0.0
Macrophages LPS	0.5	0.5	Thymus	1.5	3.0
HUVEC none	0.0	0.0	Kidney	0.1	0.0

HUVEC starved	0.0	0.0		

AI_comprehensive panel_v1.0 Summary: Ag6919 Highest expression of this gene is seen in a normal tissue adjacent to ulcerative colitis (CT=29.5). This gene is widely expressed in this panel, with moderate levels of expression in a cluster of OA samples. Thus, expression of this gene could be used to differentiate between the OA samples and other samples on this panel, and as a marker of OA. Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of OA.

General_screening_panel_v1.6 Summary: Ag6919 Expression of this gene is restricted to a sample derived from a lung cancer cell line and from the thymus(CTs=33-34). Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of lung cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Panel 4.1D Summary: Ag6747/Ag6919 Expression is highest in acutely activated T cells (CTs=25-30). This gene is expressed at higher levels during primary activation of Th2 and Tr1 cells. Thus, this gene may be important for early Th2 cell differentiation and Th2 related immune disorders such as asthma. This gene encodes a protein with homology to CD30-L, a member of the tumor necrosis factor receptor superfamily expressed on the surface of activated T cells. Thus based on this expression profile, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function. In addition, therapeutic regulation of the transcript or the protein encoded by the transcript could be important in immune modulation and in the treatment of T cell-mediated diseases such as asthma, arthritis, psoriasis, inflammatory bowel disease, and lupus.

Ag6623 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Example D: Identification of Single Nucleotide Polymorphisms in NOVX nucleic acid sequences

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be

referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

SeqCalling assemblies produced by the exon linking process were selected and extended using the following criteria. Genomic clones having regions with 98% identity to all or part of the initial or extended sequence were identified by BLASTN searches using the relevant sequence to query human genomic databases. The genomic clones that resulted were selected for further analysis because this identity indicates that these clones contain the genomic locus for these SeqCalling assemblies. These sequences were analyzed for putative coding regions as well as for similarity to the known DNA and protein sequences. Programs used for these analyses include Grail, Genscan, BLAST, HMMER, FASTA, Hybrid and other relevant programs.

Some additional genomic regions may have also been identified because selected SeqCalling assemblies map to those regions. Such SeqCalling sequences may have overlapped with regions defined by homology or exon prediction. They may also be included because the location of the fragment was in the vicinity of genomic regions identified by similarity or exon prediction that had been included in the original predicted sequence. The sequence so identified was manually assembled and then may have been extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. SeqCalling fragments suitable for inclusion were identified by the

CuraTools™ program SeqExtend or by identifying SeqCalling fragments mapping to the appropriate regions of the genomic clones analyzed.

The regions defined by the procedures described above were then manually integrated and corrected for apparent inconsistencies that may have arisen, for example, from miscalled bases in the original fragments or from discrepancies between predicted exon junctions, EST locations and regions of sequence similarity, to derive the final sequence disclosed herein. When necessary, the process to identify and analyze SeqCalling assemblies and genomic clones was reiterated to derive the full length sequence (Alderborn *et al.*, Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate DNA Sequencing. Genome Research. 10 (8) 1249-1265, 2000).

Variants are reported individually but any combination of all or a select subset of variants are also included as contemplated NOVX embodiments of the invention.

NOV1b SNP Data (CG108440-02)

Three polymorphic variants of NOV1b have been identified and are shown in Table 41A.

Table 41A. NOV1b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380440	1921	C	T	639	Ser	Phe
13378327	4730	A	G	1575	Glu	Glu
13378325	6395	T	C	2130	Tyr	Tyr

NOV4a SNP Data (CG1344340-01)

One polymorphic variant of NOV4a has been identified and is shown in Table 41B.

Table 41B. NOV4a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified

13380480	652	G	A	144	Trp	End

NOV8b SNP Data (CG137793-02)

Twenty polymorphic variants of NOV8b have been identified and are shown in Table 41C.

Table 41C. NOV8b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380443	52	T	C	9	Thr	Thr
13380444	65	G	A	14	Ala	Thr
13380445	80	G	A	19	Ala	Thr
13380446	146	A	G	41	Ile	Val
13380447	168	C	T	48	Thr	Ile
13380448	190	T	C	55	Asn	Asn
13380449	211	C	T	62	Thr	Thr
13380450	234	T	C	70	Leu	Pro
13380451	241	A	G	72	Glu	Glu
13380452	242	G	T	73	Glu	End
13380459	355	T	C	110	Gly	Gly
13380460	486	C	T	154	Thr	Ile
13380461	497	G	A	158	Ala	Thr
13380462	579	T	C	185	Ile	Thr
13380463	586	T	C	187	Thr	Thr
13380464	597	T	C	191	Val	Ala
13380465	609	T	C	195	Leu	Ser

13380466	649	C	A	208	Asn	Lys
13380467	665	A	G	214	Asn	Asp
13380468	694	A	G	0		

NOV16a SNP Data (CG138751-01)

Two polymorphic variants of NOV16a have been identified and are shown in Table 41D.

Table 41D. SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380684	70	T	C	4	Ser	Pro
13380685	411	C	T	117	Tyr	Tyr

NOV17b SNP Data (CG139062-02)

Five polymorphic variants of NOV17b have been identified and are shown in Table 41E.

Table 41E. NOV17b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380469	680	G	A	89	Gly	Gly
13380470	801	A	G	130	Arg	Gly
13380471	1178	T	C	255	Tyr	Tyr
13380475	2684	C	T	757	Tyr	Tyr
13380476	3945	G	T	0		

NOV20a SNP Data (CG140305-01)

Two polymorphic variants of NOV20a have been identified and are shown in Table 41F.

Table 41F. NOV20a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380503	218	G	T	57	Gly	Val
13380501	404	T	C	119	Val	Ala

NOV22a SNP Data (CG140843-01)

One polymorphic variant of NOV22a has been identified and is shown in Table 41G.

Table 41G. NOV22a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380504	217	A	G	57	Pro	Pro

NOV23a SNP Data (CG141540-01)

Six plymorphic variants of NOV23a have been identified and are shown in Table 41H.

Table 41H. NOV23a SNP Data

Variant	Nucleotides	Amino Acids

	Position	Initial	Modified	Position	Initial	Modified
13380496	132	A	G	22	Thr	Thr
13377809	184	A	G	40	Arg	Gly
13377810	227	C	T	54	Pro	Leu
13378253	258	C	A	64	Arg	Arg
13377812	823	T	C	253	Trp	Arg
13378251	1044	G	A	326	Thr	Thr

NOV24a SNP Data (CG14580-01)

Two polymorphic variants of NOV24a have been identified and are shown in Table 41I.

Table 41I. NOV24a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380498	197	G	A	46	Gly	Glu
13380497	1693	G	A	545	Ala	Thr

NOV26a SNP Data (CG142003-01)

One polymorphic variant of NOV26a has been identified and is shown in Table 41J.

Table 41J. NOV26a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380544	375	G	A	125	Val	Met

NOV29c SNP Data (CG171681-02)

Two polymorphic variants of NOV29c have been identified and are shown in Table 41K.

Table 41K. NOV29c SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380521	361	A	G	96	Lys	Arg
13380522	1646	G	C	0		

NOV32a SNP Data (CG52423-01)

Twenty polymorphic variants of NOV32a have been identified and are shown in Table 41L.

Table 41L. NOV32a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380557	26	C	T	0		
13380556	54	A	G	1	Met	Val
13380555	60	G	A	3	Ala	Thr
13380545	357	A	G	102	Asn	Asp
13380546	562	A	G	170	Asn	Ser
13380547	739	A	G	229	Glu	Gly
13380548	760	A	G	236	Gln	Arg
13380549	774	C	T	241	Gln	End
13380550	796	A	G	248	Asp	Gly
13380551	843	A	G	264	Ile	Val

13380552	868	T	C	272	Leu	Pro
13380553	892	T	C	280	Leu	Pro
13380554	893	G	A	280	Leu	Leu
13380542	1066	A	G	338	Gln	Arg
13380558	1073	G	A	340	Ala	Ala
13374369	1133	C	G	360	Ser	Ser
13380559	1151	G	A	366	Ala	Ala
13380560	1288	A	G	412	Lys	Arg
13380515	1303	T	C	417	Met	Thr
13374368	1357	C	T	435	Ala	Val

NOV34b SNP Data (CG55698-02)

Four polymorphic variants of NOV34b have been identified and are shown in Table 41M.

Table 41M. NOV34b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380563	170	G	A	52	Val	Met
13380564	210	A	G	65	Asp	Gly
13380565	218	C	T	68	Arg	Cys
13380566	249	C	T	0		

NOV35c SNP Data (CG55832-02)

Twelve polymorphic variants of NOV35c have been identified and are shown in Table 41N.

Table 41N. NOV35c SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380671	330	A	G	92	Val	Val
13380672	638	A	G	195	His	Arg
13380673	750	G	A	232	Val	Val
13380674	1260	T	C	402	Cys	Cys
13378289	2090	G	A	679	Arg	Gln
13380675	2100	G	A	682	Glu	Glu
13380676	3342	A	G	1096	Thr	Thr
13380677	3813	A	G	1253	Arg	Arg
13380678	4118	C	T	1355	Thr	Met
13378291	4162	C	G	1370	Gln	Glu
13380705	4397	T	C	1448	Val	Ala
13380704	5269	A	G	0		

NOV37a SNP Data (CG88634-01)

Two polymorphic variants of NOV37a have been identified and are shown in Table 41O.

Table 41O. NOV37a SNP Data

Variant	Nucleotides	Amino Acids

	Position	Initial	Modified	Position	Initial	Modified
13380706	165	T	C	22	Leu	Pro
13380707	272	A	C	58	Lys	Gln

NOV38a SNP Data (CG97012-01)

Two polymorphic variants of NOV38a have been identified and are shown in Table 41P.

Table 41P. NOV38a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380698	828	G	A	276	Gln	Gln
13380699	1271	A	G	424	Glu	Gly

5

NOV39a SNP Data (CG99754-01)

Six polymorphic variants of NOV39a have been identified and are shown in Table 41Q.

Table 41Q. NOV39a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13374727	314	T	C	100	Ile	Thr
13374728	362	G	A	116	Arg	Gln
13380709	545	C	T	177	Ser	Phe
13380710	711	G	C	232	Leu	Leu
13380711	1355	C	T	447	Pro	Leu

13380712	1886	C	T	0		

NOV40b SNP Data (CG99777-02)

Three polymorphic variants of NOV40b have been identified and are shown in Table 41R.

Table 41R. NOV40b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378112	466	A	G	126	Gln	Gln
13378113	498	A	G	137	Glu	Gly
13378114	641	G	A	185	Asp	Asn

NOV30b SAGE Expression Data

Construction of the mammalian expression vector pCEP4/Sec. The oligonucleotide primers, pSec-V5-His Forward (CTCGTC CTCGAG GGT AAG CCT ATC CCT AAC; SEQ ID NO:795) and the pSec-V5-His Reverse (CTCGTCGGGCCCCTGATCAGCGGGTTTAAAC; SEQ ID NO:796), were designed to amplify a fragment from thepcDNA3.1-V5His (Invitrogen, Carlsbad, CA) expression vector. The PCR product was digested with XhoI and ApaI and ligated into the XhoI/ApaI digestedpSecTag2 B vector (Invitrogen, Carlsbad CA). The correct structure of the resulting vector, pSecV5His, was verified by DNA sequence analysis. The vector pSecV5His was digested with PmeI and NheI, and the PmeI-NheI fragment was ligated into the BamHI/Klenow and NheI treated vector pCEP4 (Invitrogen, Carlsbad, CA). The resulting vector was named as pCEP4/Sec.

Expression of CG51117-05 in human embryonic kidney 293 cells. A 1.6 kb BamHI-XhoI fragment containing the CG5117-05 sequence was subcloned into BamHI-XhoI digested pCEP4/Sec to generate plasmid 163. The resulting plasmid 163 was

transfected into 293 cells using the LipofectaminePlus reagent following the manufacturer's instructions (Gibco/BRL). The cell pellet and supernatant were harvested 72h post transfection and examined for CG51117-05 expression by Western blot (reducing conditions) using an anti-V5 antibody. Fig. 1 shows that CG51117-05 is expressed as an approximately 66 kDa protein, secreted by 293 cells.

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims. The claims presented are representative of the inventions disclosed herein. Other, unclaimed inventions are also contemplated. Applicants reserve the right to pursue such inventions in later claims.

CLAIMS

What is claimed is:

1. An isolated polypeptide comprising the mature form of an amino acid sequenced selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

3. An isolated polypeptide comprising an amino acid sequence which is at least 95% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

4. An isolated polypeptide, wherein the polypeptide comprises an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

5. The polypeptide of claim 1 wherein said polypeptide is naturally occurring.

6. A composition comprising the polypeptide of claim 1 and a carrier.

7. A kit comprising, in one or more containers, the composition of claim 6.

8. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated

with the polypeptide of claim 1, wherein the therapeutic comprises the polypeptide of claim 1.

9. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:

(a) providing said sample;

(b) introducing said sample to an antibody that binds immunospecifically to the polypeptide; and

(c) determining the presence or amount of antibody bound to said polypeptide,

thereby determining the presence or amount of polypeptide in said sample.

10. A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the polypeptide of claim 1 in a first mammalian subject, the method comprising:

a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and

b) comparing the expression of said polypeptide in the sample of step (a) to the expression of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease,

wherein an alteration in the level of expression of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

11. A method of identifying an agent that binds to the polypeptide of claim 1, the method comprising:

(a) introducing said polypeptide to said agent; and

(b) determining whether said agent binds to said polypeptide.

12. The method of claim 11 wherein the agent is a cellular receptor or a downstream effector.

13. A method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of the polypeptide of claim 1, the method comprising:

(a) providing a cell expressing the polypeptide of claim 1 and having a property or function ascribable to the polypeptide;

(b) contacting the cell with a composition comprising a candidate substance; and

(c) determining whether the substance alters the property or function ascribable to the polypeptide;

whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a composition in the absence of the substance, the substance is identified as a potential therapeutic agent.

14. A method for screening for a modulator of activity of or of latency or predisposition to a pathology associated with the polypeptide of claim 1, said method comprising:

(a) administering a test compound to a test animal at increased risk for a pathology associated with the polypeptide of claim 1, wherein said test animal recombinantly expresses the polypeptide of claim 1;

(b) measuring the activity of said polypeptide in said test animal after administering the compound of step (a); and

(c) comparing the activity of said polypeptide in said test animal with the activity of said polypeptide in a control animal not administered said polypeptide, wherein a change in the activity of said polypeptide in said test animal relative to said control animal indicates the test compound is a

modulator activity of or latency or predisposition to, a pathology associated with the polypeptide of claim 1.

15. The method of claim 14, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

16. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of claim 1 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

17. A method of treating or preventing a pathology associated with the polypeptide of claim 1, the method comprising administering the polypeptide of claim 1 to a subject in which such treatment or prevention is desired in an amount sufficient to treat or prevent the pathology in the subject.

18. The method of claim 17, wherein the subject is a human.

19. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127 or a biologically active fragment thereof.

20. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

21. The nucleic acid molecule of claim 20, wherein the nucleic acid molecule is naturally occurring.

22. A nucleic acid molecule, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127.

23. An isolated nucleic acid molecule encoding the mature form of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

24. An isolated nucleic acid molecule comprising a nucleic acid selected from the group consisting of 2n-1, wherein n is an integer between 1 and 127.

25. The nucleic acid molecule of claim 20, wherein said nucleic acid molecule hybridizes under stringent conditions to the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127, or a complement of said nucleotide sequence.

26. A vector comprising the nucleic acid molecule of claim 20.

27. The vector of claim 26, further comprising a promoter operably linked to said nucleic acid molecule.

28. A cell comprising the vector of claim 26.

29. An antibody that immunospecifically binds to the polypeptide of claim 1.

30. The antibody of claim 29, wherein the antibody is a monoclonal antibody.

31. The antibody of claim 29, wherein the antibody is a humanized antibody.

32. A method for determining the presence or amount of the nucleic acid molecule of claim 20 in a sample, the method comprising:

(a) providing said sample;

(b) introducing said sample to a probe that binds to said nucleic acid molecule; and

(c) determining the presence or amount of said probe bound to said nucleic acid molecule,

thereby determining the presence or amount of the nucleic acid molecule in said sample.

33. The method of claim 32 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

34. The method of claim 33 wherein the cell or tissue type is cancerous.

35. A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the nucleic acid molecule of claim 20 in a first mammalian subject, the method comprising:

a) measuring the level of expression of the nucleic acid in a sample from the first mammalian subject; and

b) comparing the level of expression of said nucleic acid in the sample of step (a) to the level of expression of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;

wherein an alteration in the level of expression of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

36. A method of producing the polypeptide of claim 1, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

37. The method of claim 36 wherein the cell is a bacterial cell.

38. The method of claim 36 wherein the cell is an insect cell.

39. The method of claim 36 wherein the cell is a yeast cell.

40. The method of claim 36 wherein the cell is a mammalian cell.

41. A method of producing the polypeptide of claim 2, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

42. The method of claim 41 wherein the cell is a bacterial cell.

43. The method of claim 41 wherein the cell is an insect cell.

44. The method of claim 41 wherein the cell is a yeast cell.

45. The method of claim 41 wherein the cell is a mammalian cell.

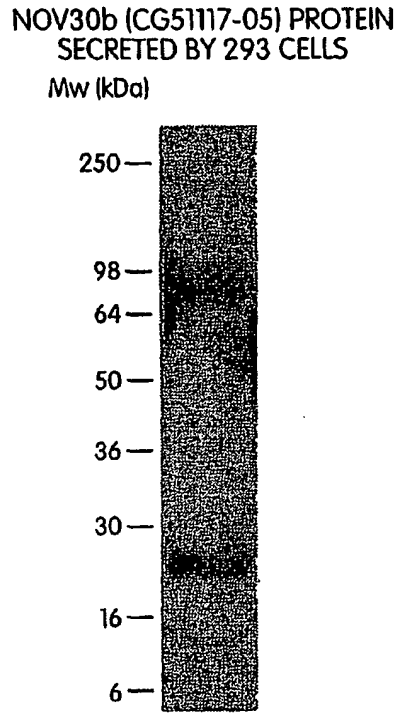
NOV30b (CG51117-05) PROTEIN
SECRETED BY 293 CELLS
Mw (kDa)
250
98
64
50
36
30
16
6

Fig. 1

NOV34b (CG55698-02) SCHEMATIC DIAGRAM OF COLIPASE AND TETRA EHTYLENE GLYCOL MONOOCTYL ETHER INHIBITOR

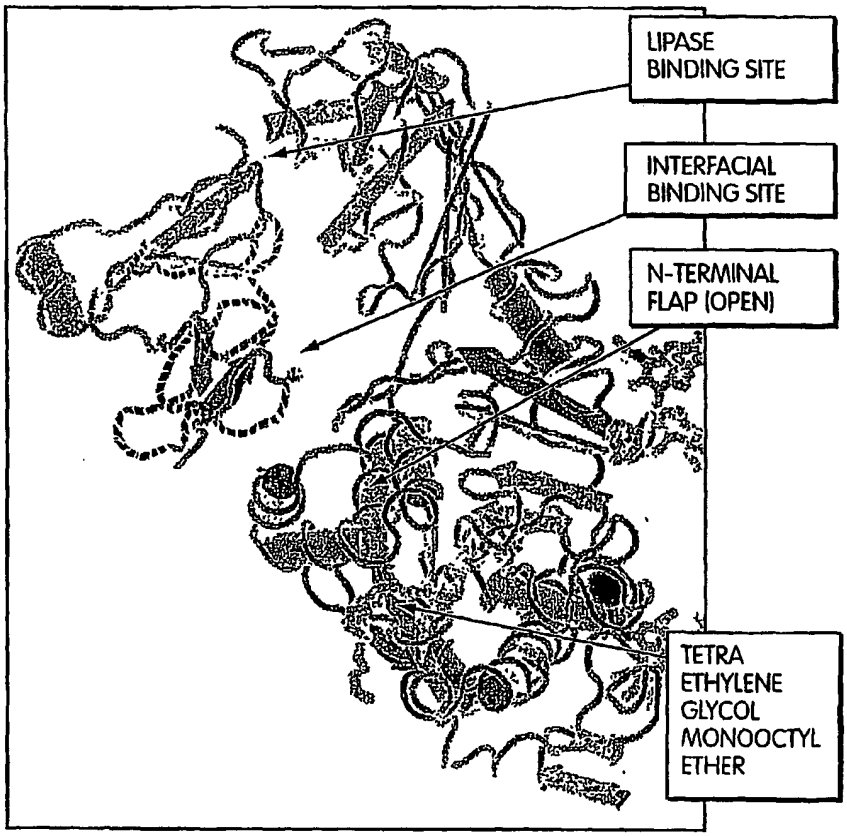

Fig. 2

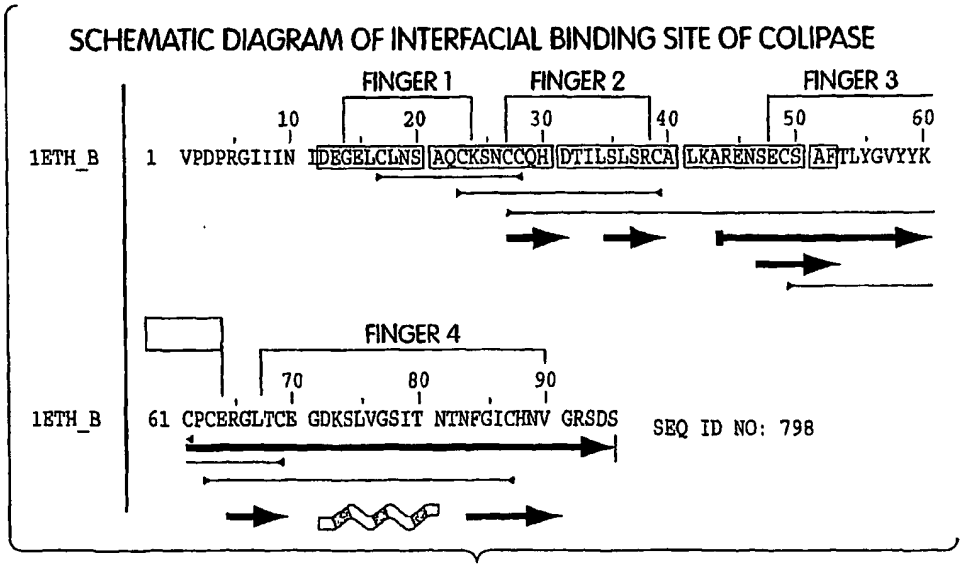
SCHEMATIC DIAGRAM OF INTERFACIAL BINDING SITE OF COLIPASE
FINGER 1
FINGER 2
FINGER 3
10
20
30
40
50
60
1ETH_B
1 VPDPRGIIIN IDEGELCLNS AQCKSNCCQH DTILSLSRCA LKARENSECS AFTLYGVYYK
FINGER 4
70
80
90
1ETH_B
61 CPCERGLTCE GDKSLVGSIT NTNFGICHNV GRSDS
SEQ ID NO: 798

Fig. 3

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13*ter*.1(c) and 39)

Applicant's or agent's file reference 21402-442A	**IMPORTANT DECLARATION**	Date of mailing (day/month/year) 17 MAY 2005
International application No. PCT/US02/28596	International filing date *(day/month/year)* 09 September 2002 (09.09.2002)	(Earliest) Priority date *(day/month/year)* 06 September 2002 (06.09.2002)

International Patent Classification (IPC) or both national classification and IPC

IPC(7): C07K 1/00, 14/00; C07H 21/02, 21/04; C12P 21/06 and US Cl.: 530/ 350, 300; 536/ 23.1, 23.5; 435/69.1

Applicant

CURAGEN CORPORATION

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
   - a. ☐ scientific theories.
   - b. ☐ mathematical theories
   - c. ☐ plant varieties.
   - d. ☐ animal varieties.
   - e. ☐ *essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.*
   - f. ☐ schemes, rules or methods of doing business.
   - g. ☐ schemes, rules or methods of performing purely mental acts.
   - h. ☐ schemes, rules or methods of playing games.
   - i. ☐ methods for treatment of the human body by surgery or therapy.
   - j. ☐ methods for treatment of the animal body by surgery or therapy.
   - k. ☐ diagnostic methods practised on the human or animal body.
   - l. ☐ mere presentations of information.
   - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
   ☐ the description ☐ the claims ☐ the drawings

3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:
   - ☐ the written form has not been furnished or does not comply with the standard.
   - ☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:

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(54) Title: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

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(15) **Information about Correction:**
see PCT Gazette No. 43/2005 of 27 October 2005, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13*ter*.1(c) and 39)

Applicant's or agent's file reference 21402-442A	**IMPORTANT DECLARATION**	Date of mailing (day/month/year) 17 MAY 2005
International application No. PCT/US02/28596	International filing date *(day/month/year)* 09 September 2002 (09.09.2002)	(Earliest) Priority date *(day/month/year)* 06 September 2002 (06.09.2002)
International Patent Classification (IPC) or both national classification and IPC IPC(7): C07K 1/00, 14/00; C07H 21/02, 21/04; C12P 21/06 and US Cl: 530/350, 300; 536/23.1, 23.5; 435/69.1		
Applicant CURAGEN CORPORATION		

This International Searching Authority hereby declares, according to Article 17(2)(a), that *no* international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
   - a. ☐ scientific theories.
   - b. ☐ mathematical theories
   - c. ☐ plant varieties.
   - d. ☐ animal varieties.
   - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
   - f. ☐ schemes, rules or methods of doing business.
   - g. ☐ schemes, rules or methods of performing purely mental acts.
   - h. ☐ schemes, rules or methods of playing games.
   - i. ☐ methods for treatment of the human body by surgery or therapy.
   - j. ☐ methods for treatment of the animal body by surgery or therapy
   - k. ☐ diagnostic methods practised on the human or animal body.
   - l. ☐ mere presentations of information.
   - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
   ☐ the description ☐ the claims ☐ the drawings

3 ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:
   - ☐ the written form has not been furnished or does not comply with the standard.
   - ☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:

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